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                                                                                                                                                                                                                               Query Match
Hest Local Similarity
                                                                                                                                                           Matches
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InterPro: JPR00350b; Jq_like.
InterPro: JPR00359b; Jq_v.
InterPro: JPR00034; Laminin_K.
InterPro: JPR002049; Laminin_EGF.
InterPro: JPR001791; Laminin_EGF.
InterPro: JPR001791; Laminin_CG.
InterPro: JPR002172; LDL_recept_A.
InterPro: JPR00082; SEA.
Pfam: PF00052; Laminin_B; 3.
Pfam: PF00054; Jaminin_EGF; 8.
                                            2293
                                                                                                   2234
                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART:
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[2]
                                                                                                                                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS50068; LDLRA_2; 4.
                                                                                                                                                                                                                                                                                                  SMART; SM00192; LDLa; 4. SMART; SM00200; SEA; 1.
                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00057; 1d1_recept_a; 4. Pfam; PF01390; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicole S., Davoine C.S., Topaloglu H., Cattolico L., Harral D.,
Heighton P., Hen-Hamida C., Hammouda H., Cruaud C., White P.S.,
Samson D., Urtizberca J.A., Lehmann-Horn F., Weissenbach J.,
Hentali F., Fontaine H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDIANE 20553141; Pubmod 11101850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   PROSITE; PS00022;
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD003031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL445795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Perfecting the major proteoglycan of basement membranes, is aftered patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).
                 03.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEPAKAN SULFATE PROTECGLYCAN PERLECAN (FRAGMENT).
HSPG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID+9606;
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#
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIVMOGI (VATICEL)
                                        SNGMEAS - - I TVTVTGTQGANLAY PAGSTQP1 R1EPSSSQVAECQTLDLNCVVPGQSHAQ
                                                                     TQGITSSGTASLTFEGTLGA-------P1-1PKTSSKYFNFTTED-------
                                                                                                                            TI VDQTNVKLTCLLFSGNYEALPI I YKNGDI - - - - - VRFHRLKI - - - - - -
                                                                                                                                                                                                                                                                                                                                                       1: SM00181; EGF; 15.
1: SM00180; EGF_Lam; 12.
1: SM000180; EGF_Like; 7.
1: SM00009; EGF_Like; 7.
1: SM00409; IG; 22.
1: SM00408; IGC2; 22.
1: SM00408; IGC2; 12.
1: SM00408; IGC; 1CV; 7.
1: SM00410; IG_Like; 1.
                                                                                                 TVAEGQTEDESCVV - AGQAHAQVTWYKRGGSEFARHQVRGSKEYT FQASPADAGQYVCKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genet. 26:480-483(2000)
                                                                                                                                                                                                                                                                                                                              SM00282; LamG;
                                                                                                                                                                                                                                                                                                                                             SM00281; LamB;
HKMVEALIRAWASTHMSPSWTILLKI,CHVQFMQYFDL/TCQLIAGKAFVINASTELLKVWDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00261;
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                                                                                                                                                                                                                               4370 AA;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDLRECEPTOR.
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                                                                                                                                                                                                                               466592 MW; FBD762C3940A657C CRC64;
                                                                                                                                                                    5.8%; Score 102.5;
24.3%; Pred. No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_2.
                                                                                                                                                          39; Mismatches
                                                                                                                                                                     16.
                                                                                                                                                                                      DF 4;
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                                                                                                                                                                                      Length 4370;
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RESULT 13
004538
1D 00
AC 00
DT 01
DT 01
DT 01
DT 81
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Best Local Similarity
Matches 48; Conserv
         01-JUL-1997 (TrEMBLEC). 04, Greated)
01-JUL-1997 (TrEMBLEC). 04, Last sequence update)
01-JUL-1997 (TrEMBLEC). 17, Last annotation update)
01-JUN-2001 (TrEMBLEC). 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMirray A.A.:

Submitted (NOV-1996) to the EMBL/GenBank/DDR3

EMBL: AL052671; CAA21777.2; -

EMBL: AL05268; CAA21777.2; JOINED.

EMBL: 281568; CAB76729.1; -

EMBL: AL032671; CAB76729.1; JOINED.

EMBL: AL032671; CAB76729.1; JOINED.

EMBL: AL032671; CAB76729.1; JOINED.

EMBL: AL032671; CAB76729.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CMXME2;
01-NCV-1995 (TLEMBLECT, 12, Created)
01-NCV-2000 (TLEMBLECT, 13, Last sequence update)
01-CCT-2000 (TLEMBLECT, 15, Last annotation update)
485. I PROTEIN.
                                                                        004738;
                                                                                    004538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis,
NCHI_TaxHP-62-0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlow K
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                                                                                                                                                            196
                                                                                                                                                                                                                   1.39
                                                                                                                                                                                       319 VSLRP
                                                                                                                                                                                                                                  160 QYFDLTCQLLGKAEVDGASFILKVWIXTK********TPFPSWRVLJQDLV 202
                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                            VPEEP
                                                                                                                                                                                                                                                                                           LEGDLSHTHKLONLITIDTLYYINHVHVAKSLKVGSFLKTYSLHTKLOSMNSENOFMLSLE
                                                                                                                                                                                                                                                                                                                                  OYFDLLAQVHSVVETMDGLWMLRVWRAQKFGPES1KERKERQLFHVTQFSFKRY1VPPNF
                                                                                                                                                                                                                   --LHGGGEAYORG1STVF VDEEVDAFONFKRKVESVLENVLYDENF1EFQOPEEVTENK
                                                                                                                                                                                                                                                                         RIGKATEEFGKEYL-1EINVYDEHRADLVSLNSGNFVAIQNVHA-ASTPHREIQ1-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSASLANGHTLDLNCLVASQAPHTTTWYKRGGSLPSRHQTVGSRLRTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLKYGSFLRI -----YSLHTKLOSMNSENOTMLSLEFHLHGGTSYGRGIRVLPES
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                                                                                                                                                                                       323
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRITTIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    5.7%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25209 MW; BE4975C081625390 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100.5;
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                                                                                                                                                                                                                                                                                                                                                                                                       No. 0.43;
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F20P5.20.

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                                                                                                                                                                                                                                    191 FPSWR----VLIQDLVLEGDLSH--INRLQNLTIDILVYDNHVHVAR---SLKVGSFLRIYS 243
                                                                                                                                                                                                                                                                                               251 ASAARPADAYPEDNNPEAAQQHPWVGPYGRRTIQISCYDAHADFIREAGVSAGMWLSLRN 310
   ---RVWASTHM 144
                                                        133 IPVYPASAQVALLPPKOGESHKLLKEEHHQYVSYLYNVIDKYDVPDEAEYQQRVKVSLNV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 YPDVLAQVIISVVETKNGSWTLRVWRAQKFGPEASKEK----REMNLFHVTENTFKCYIVP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 DDHRIGIEKLNSGDFVALONVHAASVGLTEMOVLHG------GGOAYNRGISK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 109; DB 5; Length 587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kershaw J.;
Submitted (OCT-1996) to the EMBL/Genhank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LPES--NSDVDQLKKDLESA-----NLTANQHSDVICQSE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 VPVDFRNEAFQIFKRRVESVLEAVTDCDNFIEFQQKENVVQSE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
F39H2.1 PROTEIN.
112 APIT-----PRTSSKYFNFTTEDHKMVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 0.31;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 PDPRIGKAVEESGKEFL.....
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                                                                                                                145 SPSWTLLKLCDVQPMQYFDLTCQL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        244 LHTK 247
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MEDLINE-98290545; Pubmed-9628581;
Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 FEGTLGAPTIPRTSSKYFNFTTEDHKMVEALRVWA---STHMSPSWTLLKLCDVQPMQYF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 DEFCOLLGRAEVIOGASFELIKVW----PGTRTPFPSWRVLLQDIALEGDESH [HRLQNET ID 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 DLIGOLEYK-DCHALDQWRKGWFAMDKSSLIIF-----CLOMOEVOGDRMHLRRLOELFTS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 IVOQTNVKLTCLL5---FSGNYEALPLIYKNGDIVRFHRLKIOVYKKETQGITSSGFASLT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                               "Prediction of the coding sequences of unidentified human genes. IX the complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
                                                                                                                              Homo sapions (Human).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Eutoleostomi;
Mammalla; Eutheria; Primates; Catarrhinl; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 TMVQNGEKLDVLLLVEKGRTEYTHG-HTKLDFTVWHTALEKAAGTDGNALQDQQLSKNDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 MLSLEFHLHGGTSYGRGIRVLPESNSD-----VDOLKKDLESANLTANOH 302
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                                                                        Last sequence update)
Last annotation update)
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(Trimblrel, 16, Last sequence update)
(Trimblrel, 17, Last annotation update)
                              1044 AA.
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                                                            Created)
                              PRT;
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Pfam; PP00620; RhoGAP: 1.
Pfam; PP01412; ArfGap; 1.
PR1NTS; PR00405; REVINTACTING.
PROSITE; PSSSGGN1: PI_DOMAIN; 3
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KIAA0580 PROTEIN (FRAGMENT)
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nes 70; Conservative
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                                                          01-NOV-1999 (TrEMBLrel.
                                                                          (TremBLrel.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-ADG-2000) to the DDRJ/EMRL/GenBank databases. Takao Isroani Herisk Research Institute, Genomics Laboratory; 1532-3 Yana Kisaraare 'Niba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-435- 3951, Fax:81-438-52-3952)
NEDO human CDNA - Omencing project supported by Ministry of NEDO human CDNA - Omencing project supported by Ministry of
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Homo sapiens teratocarcinoma cell_line:NT2 cDNA
clone_lib:NT2RM2 clone:NT2RM2001805.
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Isoqai, T. and Otsuki, T.
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Homo sapiens cDNA FLJT2518 fis, clone NT2KM2001805
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id+"bah14110.1"
/protein_id+"stan41618"
/db_xref+"Cl:10434051"
/translation+"mst.PpAnTw1YTPLNOLKGGTJVNVYGVVKFFKPPYLSKGTDYC
/translation+"mst.PpAnTw1YTPLNOLKGGTJVNVYGVVKKETQGJTSSGFA
SVVTTVDQTNVKLTCLLFSGNYEALPJJYKNGDJVRFHHLKJQVYKKETQGJTSSGFA
                                                                                                                                                                                                                                                                                                                                                                           /note="cloning vector: pME18SFL3-mRNA from uninduced neuronal precursor cells." 439.\ .2343
                                                                                                      Q1PASEVLMDDDLQKSVDM1MDMFCPPG1K1DAYPWLECF1KSYNVTNGTDNQ1CYQ1
                                                                                                                       CLLL1 EGGTLSE1CKLSNKFNSY I PVKSCHEDLELLDLSAPFL1QGT1HHYGCKQCSS
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/codon_start=1
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/clone-"NT2kM2001805"
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/db_xref="taxon:9606"
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LOCUS	LOCUS DEFINITION	AK001935 2077 bp mRNA PRI 22-FEB-2000 Homo sapiens cDNA FLJ11073 (is, clone PLACE1005026.	qo	
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SOU		Homo sapiens placenta cDNA to mRNA, clone_tib:PLACE1 clone:PLACE1005026,	qu	311 CTCTTTAGTG
T	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi:	ζ	24.1 tttcacaqqet
485		Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (sites)	d.	371 TTTCACAGGC
<	AUTHORS	Isogal, T., Ota, T., Hayashi, K., Suqiyama, T., Otsuki, T., Suzuki, Y.,	7.0	301 tttgcatctt
		Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamanosu,J.,	qc	431 TTTGCATCTT
Ļ	TITLE	wakamatsu,A., Nakamura,Y., Naqahari,K., Masuno,Y. and Sasaki,N. NEDO human cDNA sequencinq project	ογ	361 aagtatttta
L.	JOURNAL	Unpublished (2000)	f	
<		Lsogal, T. and Otsuki, T.	3	W111 101000 101
E- **	TITLE	Direct Submission Submitted (16-PFR-2000) to the DDRJ/EMBL/GenBank databasess fakeo	ΛO	421 tetaeteatat
		Isoqai, Helix Research Institute, Genomics Laboratory: 1532-3 Yana,	qa	551 reractearn
į		risardau, chiba 252-0012, Japan (r. mart. genomics mr. 1. co. jp.) Tel:81-438-52-9951, Fax:81-438-52-3952)	07	481 tattttgacct
E	COMMENT	NEDO NUMBA CDNA Sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA 1011 insert	qu	611 TATTTGACC
		Sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection;	ΛO	541 ctaaaqqtab
		Helix Research Institute (supported by Japan Key Technology Center		
		etc.) and Department of Virology, institute of Medical Science, University of Tokyo.	g _C	671 CTAAAGGTAT
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Bonfield J., Burton J., Connell M., Copsey T., Coper J.,
Craxton M., Dear S., Du E., Durbin K., Favello A., Fulton
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Caenorhabditis elegans
                                                                                                                      SEQUENCE FROM N.A. MEDLINE-94150718; PubMed-7406398;
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Haynes C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1998) to the EMBL/GenBank/DDBJ EMBL: AF067831; AAC27615.1; -. HSSP: P29549; lOTC.
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"Oxytricha trifallax macronuclear alpha telomere binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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Eukaryota: Alveolata: Ciliophora: hypotrichs: Stichotrichida:
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2307; Telo_bind_alpha; 1.
497 AA; 56361 MW; 132C76
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larity 21.9%; Fred. No. 0.00019;
Conservative 57; Mismatches 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
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132C768D6C3AB686
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Rest Local Similarity 25.7
Matches 52; Conservative
                                                                                                                              Matches
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Best Local Similarity
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03-JUN-2001 (TrEMBLECT: 17,
01-JUN-2001 (TrEMBLECT: 17,
01-JUN-2001 (TrEMBLECT: 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lidthinin J., Lloyd C., Menurray A., Mortimore B., C'Calladhan M., Parsons J., Percy C., Kirken L., Roopra A., Saunders D., Shownkeen Parsons J., Fercy C., Kirken L., Roopra A., Sunders D., Shownkeen Smalaon N., Smith A., Sonnhammer E., Staden A., Sudston J., Thomas K., Vaudin M., Yaughan K., Waterston K., Waterson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; C. 2000 Contiguous nucleotide sequence from Chromosome III of C.
                                                                                                                                                                                                       German Neurospora genome project;
Submitted (FEE-2001) to the EMBL/GenBank/DDB3
EMBL: AL513442; CAC28643.1; *
SEQUENCE 759 AA: 85218 MN; DC737A5574FF4F
                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota; Fund; Ascomycota; Perizomycotina;
Sordariales; Sordariaccae; Neurospora.
NCB1_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Schulte O., Aign V., Hoheisel J., Brandt P.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
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EMBL; Z83110; CAR05525.1;
SEQUENCE 251 AA; 28987
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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 DESAGMENT I
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6; Pred. No. 0.0013;
30; Mismatches 60
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Pred. No. 0.29;
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Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F., Gustincia M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombacris P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 IYKNGDIVRFHRLKIQVYKKETQGITSSGFA-----SLTFEGTLGAPIIPRTS---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SKYFNFTFDHKMVEALRVWAS----THMS-PSWTLLKLCDVQPMQYFDLTC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKOVGOPLILING ITLRSYRDRYGGLSKDOFRYALWPDFSSNSKDTLCPOPMPRLMKTGDK 157
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                          1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTfVDQTNVKLTCL 60
                                                                                                                                                                                                                                                                                      Sdry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 KKNTIVNLFGIVKDFTPSRQSLHGTKDWYTVYLWLDPTCDTSSIGLQIHLFSKQGNDLPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGGT1VNVYGVVKFFKPPY1,S-KGT-DYCSVVT1VDQT----NVKLTC11,FSGNYEA1,P1-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEQFALLLNK IWDEOTNKIIKNGELLSTSSARONQTGLSYPSVSFSLLSQ ITPIIQRCSFYA
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                                                                                                             Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299126; CAB16192.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 555;
                                                                                                                                                                                                                     Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Mismalches 118; Indels
                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1999 (TrEMBLrel. 09, Created)
01-MAY-2000 (TrEMBLrel. 13, Last soquence update)
01-MAY-2000 (TrEMBLrel. 13, Last annolation update)
HYPOTHETICAL 64.1 KDA PROTEIN C26H5.06 IN CHROMOSOME I.
SPACZ6H5.06
                                                                                                                                                                              08BBB9FC5D0C7088 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungl; Ascomycota; Schlzösaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                     Score 324; DB 11;
Pred. No. 2.7e-21;
6; Mismatches 17;
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24.4%; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                          555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                            61 LFSGNYEALPIIYKNGDIVRFHRLKI 86
                                                                                                                                                   EMBL; AK013364; BAB28810.1; -. MGD; MGI:1920086; 2810458H16Rik.
                                                                                                                                                                               12740 MW;
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73.3%;
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                                                                                                                                                                                                                                                63; Conservative
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es 77; Conserva
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Best Local Similarity
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                                                                                                                                                                               SEQUENCE
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Ol-MAR-2001 (TrEMBLrel. 16, Last annown-01-MAR-2001 (Marchadopsis, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                           262 SIRCILWDEHDFYCRNYIKEGDYVVMKNVFTKIDHLG------YLECILHGDSAKRYNM 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 FHRLKTOVYKKETOG1----TSSGFASLTFEGTLGAPT1PRTSSKYFNFTTFEDHKMVEAL, 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 LSRVKTVLTNRKTTALCNETTSSSPA - - LENGKHSVDS EPYOSSPRFT,MREODKNFT,SNL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006700; BAB08953.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 VNVYGVVKFFKPPYLSKGTDYCSVVTIVD--QTNVKLTCLLFSGNYEALPITYKNGDIVR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 TIDILVYDNHVHVARS-LKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTS--YGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 VNLIGVIVELG -- FSNGSDCSCTLK IVDPWYSGSGLPVKFVART [RDLPRVESIGDIIL]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 RVWASTIIM----SPSWTLLKLCDVQPMQYFDLTCOLLGKAEVDGASFLLKVWDGTRTPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 VDRVSEKOATHCLO-----PGOHVKLL----NLFFOVNMGLMNATFTPSTKMOYTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.) SWRVELIQD----LVERGDESHTHREGNETEDTEVYDNHVHVARSEKVGSPERTYSERFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 OSMNSENOTMI, SLEFIILHGGTSYGRGTRVI, PESNSDVDOLKKDI, ESANI, TANQHSDVTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E.,
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Last annotation update)
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23.7%; Pred. No. 2.8e-05;
ive 49; Mismatches 138
                                                                                                                                                                                                                                                                                         463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 SEPDDSEPNGVSLRP------PGWSSVAR 331
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(TrEMBLrel. 17, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53630 MW;
                                                                                                   274 GIRVLPESNSDVDQLK 289
                                                                                                                                            315 SIEKVDSEEPELNEIK 330
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15;
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ANGESTRAL CALCIUM SITE.

BP-HAND 1 (POTENTIAL).

IRON (BY SIMILARITY).

IRON (BY SIMILARITY).

IRON AND MANGANESE (BY SIMILARITY).

MISSING (IN ISOFORM 1B).

IIDILUASDPRANGCEPHYCR -> SGYYGRORHODIKRES IDILUASDPRANGCEPHYCR -> SGYYGRORHODIKRES IDILUASDPRANGCEPHYCR -> SGYYGRORHODIKRES IDILUASDPRANGCEPHYCR -> SGYYGRORHODIKRES IDILUASDPRANGCEPHYCR -> SGYYGRORHODIKRES IN ISOFORM 2).

MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SKYFNFTTED----HKMVEALR---VWASTHMSPSWTLLKLCDVQ-----PMQYFDLTC- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 -----QLLGKAEVDGASFLLKVWDGTRTPF------PSWRVL[-----QD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 L. ......VI.EGDL. ----SHTHRLONETTD11,VYDNHVHVAR ----- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 SLKVG---SFLRIYSLHTK--LOSMNS------ENOTMLSLEFHLHGGTSYGRGI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 NLRYGETREILHKYKLHGKRILOILEEFYAMLPIGTIVDNEILV-----HGGISETFDE, 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Indels 105; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 RVL······PESNSDVDQLKKDLESANLTANQHSDV1CQSEPDD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.0%; Score 88.5; DB 1; Length 653; Best Local Similarity 21.5%; Pred. No. 7.2; Matches 63; Conservative 32; Mismatches 93; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                 K -> T (IN REF. 2).
DF7B78C444EE6484 CRC64;
                                                                                                                                Hydrolase; Calcium-binding; Magnesium; Iron; Repeat;
Ptam; PF00612; IQ; 1.
Pfam: PF00149; STPhOsphatase; 1.
PRINTS; PR00114; STPHPHTASE.
SMART: SM00054; EFh; 2.
SMART; SM00156; IQ; 1.
SMART; SM00156; PP2Ac; 1.
PROSITE; PS00128; EF_HAND; 2.
PROSITE; PS00129; SER_THR_PHOSPHATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                      653 ML
417 MI
367 K
75792 MW;
                                                                                                                                         Alternative splicing.
DOMAIN 121 43
DOMAIN 121 650
CA_BIND 579 590
CA_BIND 619 630
METAL 172
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172
174
201
233
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234
285
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132
355
376
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356
367
653 AA;
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METAL
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Search completed: April 9, 2002, 17:11:15 Job time: 244 sec

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RESULT PREZIMENT OF CONTROL OF CO
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                                                                                          1_HUMAN
PPEI_HUMAN STANDARD: PRE: 654 AA.
PPEI_HUMAN STANDARD: PRE: 654 AA.
C14829: O15253; O9UJHO; O9NUZ1:
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
SERINE/THREONINE PROTEIN PHOSPHATASE WITH EF-HANDS-1 (PPEF-1) (PROTEIN DHOSPHATASE WITH EF-CALCHM-HINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communerial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: 1PR001516; Oxidored_q1_N.
Priam; PF00361; oxidored_q1; 1.
Priam; PF00662; oxidored_q1_N; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 570 AA; 65196 MW; 2363671P*1P*4C4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the mitochondrial genome of Paramecium.
Nucleic Acids Res. 18:17:180(1990).
-:- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
                  Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMB1.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-STOCK 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to licensemish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venuti S.E., Cummings D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pritchard A.E., Seilhamer J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion
                                                           PPEF1 OR PPEF OR PPP7C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; 1Pk001750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIK; S07744; S07744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramecium tetraurelia.
                                                                                (SERINE/THREONINE PROTEIN PHOSPHATASE 7) (PP7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                        257
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                                                                                                                                                                                                                                                                                                                      ----IHSATLVSAGVELIMREYPILELSLYFKL
                                                                                                                                                                                                                                                                                                                                                              VYDNHVHVARSLKVGSFL--RIY-----SLHTKL 248
                                                                                                                                                                                                                                                                                                                                                                                                      ----LLFAAFVKSAQFGFHVWLPDSMEAPVPASAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                        LTCQLLGKAEVDGASFLLKVW--DGTRTPFPSWRVLJODLVLEGDLSH1HRLONLTIDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPIIYKNGDIVAFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPKTSSKYFNFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSFTLLT-LT1GVFVNLYTYSYFKYEPH1SK-----L1SL1NAF1ASM11LVNSGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSAVLIALILIYANVHDLNFEAILNVSHLYSEMKLGSTPQ1NSWNL1SFC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Primates;
                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.0%;
21.2%;
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(-)
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  Catarrhini;
                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahalingam K., Sable C.L.,
  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75; Indels 106;
                       Euteleostomi;
                                                                                                     (EC 3.1.3.16)
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      Gratham D.:
                       InterPro:
                                                                                  300109;
                                                                                                                          AL096700;
                                                                                                                                                                AF027977;
                                                                                                     P08129: 1FJM
                                                                                                                                             Z94056; CAR40074
                       1PR000048;
1PR000934;
                                                               IPR002048; EF-hand
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"Molecular cloning, expression, and characterization of a novel human scrine/threonine protein phosphatase, PP7, that is homologous to Drosophila retinal degeneration C gene product (idgC).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinal degeneration C (rdgC) gene is neurons of neural crest origin."; Hum. Mol. Genet. 6:1437-1445(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montini E., kudarti E.J., van de Vosse E., Andolfi G., Mariani M.,
Puca A.A., Consales G.G., den Dunnen J.T., Bullabio A., Franco B.,
"A novel human serine-threonine phosphatase related to the brosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND
TISSUE-Fetal brain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine/threonine phosphatases
degeneration C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-ketina;
MEDLINE+97471020;
                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                              use by non-prolit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as Jong as i
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-355 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE-98104127; PubMed-9430683;
Huang X., Honkanen K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97358589; PubMod:9215685
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"Identification and characterization of a conserved family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCH1_Tax ID-9606;
                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: DETECTED IN RETINA AND RETINAL DERIVED TISSUE SPECIFICITY: DETECTED IN RETINA AND RETINAL DERIVED RETINOBLASTOMA CELLS. ALSO FOUND IN FETAL BRAIN.

SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.

SIMILARITY: CONTAINS 1 IO DOMAIN.

SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1 (8 ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: MAGNESIUM.
ENZYME REGULATION: ACTIVATED BY CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
                                                                                                             AF023455; AAH82795.1; -.
                                                                                X97867: CAA66461.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acad.
CAA6646].]; ...; AAC05825.]; ...
CAH40074.]; ...
CAB86407.]; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE
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AY HAVE
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Sen_thr_phosphtse

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15;
                                                                                                                                                                                                                                                                                                                  88 VYKKETOGITSSGFASLTFEGTLGAPIIP-----RTSSKYFN------FTTE 128
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                                                                                                                                                                                                                                                                                                                                                                           DHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFLLKVWDGTR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                89 TPFPSWRVLIQDL-----VLECDLS------HIHRLONLTIDILVYDNHVHVARSLKV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 GSFLRITSLHTKLOSMNSENQT-MLSLEFHLHGGTS-------YGRGTRVLPE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavaue A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nut., nn D.T., Utterback T.R., Sandek D.M., Phillips C.A., Merrick J.M. Tomb J.F., Dougherty B.A., Bott K.P., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III. Venter J.C., "The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                      205 KPRKLMDFSDNCALILEDDRSDISSTCANNINHNTELLPTELDTLVGKG---RF---AE 257
                                                                                                                                                                                                                                                                                                                                                                                                     312 ERKTEMGKQYWLITAFHAKGNLQEYLTRHVISWEDL--RKLGSSLARGIAHLHS--DHTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 CGRPKMPIVHRDLKSSNILVKNDLFCCLCDFGLSLRLDPTLSVDDLANSGOVGTARYMAP 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EVIESRMNIENMESFKOTDVYSMALVIWEMTSRCNAVGEVKDYEPPFGSKVREHPC 483
                                                                                                                                                                                                                                                           33 KPPYLSKGTDYCSVVTIVDQTNVKLTCL-LESGNYEALPI----IYKNGDIVRFHRLKIQ 87
                                                                                                                                                                                                                                77;
                                                                        (POTENTIAL)
                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria: Firmicules; Bacillus/Clostridium group; Mollicutes; Mycoplasmatacae; Mycoplasma.
NGBL_TaxID-2097;
                                                                                                                                                                                                     Length 567;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 18530 / G-87;
MEDLINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison G.A. III;
                                                                                                                                                          EC1D7642A51A3B75 CRC64;
             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.

N-LINED (GLCUNAC. . . ) (I
N-LINED (GLCUNAC. . . ) (K
N-S RS (IN REF 2).
 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                              Mismatches 136;
                                                                                                                -> G (IN REF. 2).
-> S (IN REF. 2).
-> R (IN REF. 2).
                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THYMIDINE PHOSPHORYLASE (EC 2.4.2.4) (TDRPASE) DEGO OF MGOSI.
                                                                                                                                                                                                     5.0%; Score 89.5; Di 20.7%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA
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STRAIN-ATCC 31530 / G-37;
MEDLINE-96026346; Pubmed-756993;
                                                                                                                                                                                                                                51;
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P47297; 049312;
01-FEB-1996 (RCL. 33, Created)
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MM
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                                                                                                                                                            64241
                                                                                                                                                                                                                                 Conservative
 5567
546
258
2277
379
70
94
389
4403
4405
                                                                                                                                                         567 AA;
                                                                                                                                                                                                                  Local Similarity
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94
388
403
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CARBOHYD
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                            FUNCTION: THE BUXIMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
OF PYRINIDINE MUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
OR IN THE RESCUE OF PYRINIDINE BASES FOR NUCLEOTIDE SYMTHESIS,
CATALYTIC ACTIVITY: THYMIDINE + PHOSPHATE - THYMINE + 2-DEOXY-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 FYK ----NGD FVRF-HRLK LOVYKKETOGT ------TSSGFASLFFEGTLAAPT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 IPRTSSKYENFTFEDHKMVEALRVWASTHMSPSWFLLKLKLOVOPMOYFDLT -OOLLKK - 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 VAKESGRGT,GYTGGT1DKIJRAVGV------KTELTDQQAQACIJDKNDXF11GQSK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 DIAPVDKVLYGLRDTTGTVDSLP----LIASSIMSKKIA------VMNEY1FT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 ENQEKGGTIVNVYGVVKFFKPPYLSKGTDYGSVVTIVD-OTNVKLFCLEFSG-NYEALPI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 INKKORGKALNL-AEINWFVNAVLNK-----TIADYQUTAFLMAIWFKGMNPNELFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 LTKAMVDTGETTKFNIHGKTSVDKHSTGGTGDKVSLALVPTLTSLGFS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 DLAYGKGAPGWTKKTANELAKLAGSTAKSFKRIJSVKLS-DMNOVIGKAVGNVTEVNEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- AEVDGASFELLKVWDGTRTPFPSWRVLTQDLVLEGDLSHTHRLQNLT1D11,VYDNHVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 ARSLKVGSFLRTYSLHTKL----OSMNSENOTMLSLFFHLJRGTTSYGRGTRVLPESNSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                         RIBOSE 1-PHOSPHATE.
SUBJUICT: HOMODIMER (BY SIMILARLITY).
SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES FAMILY.
survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%; Scott 19: 08:1; Length 421; (2.1%; Pred. Ro. 3.5;
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46355 MW; 649CD517CD6E5E62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interproj PR003262; Anthr_phosphorbsyllransf.
InterProj PR000312; Glycos_transf_3.
InterProj PR000033; Thymid_phosphis.
Promy PR000991; Glycos_transf_3; I.
ProDom; PD001864; Glycos_transf_3; I.
ProDom; PD005916; Thymid_phosphis; I.
PROSTRE, PS00647; THYMId_phosphis; I.
PROSTRE, PS00647; THYMID_PHOSPHORYIASE; I.
CANTELLER LETASE; Glycosyllransterase; Complete protecome.
CONFLICT 392 V -> I (IN REF. 2).
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NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
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01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update
                                         Bacteriol, 175:7918-7930(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U39684; AAC71267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U02191; AAD12476.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                         sequencing.
J. Bacterio
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P15584;
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J. Mo): Evol. 32:105-12:(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJINE-91178815; PubMed-1706781;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALA: FAMILIES CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONCEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identifying coding exons by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WITH
PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD HE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                              CODING NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALES I GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVE. THANSCRIED BY POLITIE NORMAL TRANSCRIETS BAY CONTAIN ALL DEFINE. PUBLICIES IN 5 OR 5 INFRANSLATION BEGINS. HOWEVER, CLAS LIBRARIA, AND CHEMICAL PARTICLAL AND ORIENTATION. ALTHOUGH ALL ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THAT ALU REPEATS FALL INTO 8 SUBFAMILIES: THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE HEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF FACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELL NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEPEATS
                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLLUTION OF PROTEIN SEQUENCE DATAHASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371:752-752(1994)
                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u family developed through successive waves of fixation connected with primate lineage history.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONSEQUENCE OF ERRONEOUS ALD-DERIVED AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evol. 27:194-202(1988).
                                                                                                                                                                                                                                                                            and this statement is not removed.
                                                                                                                                                                                                                                                                                               non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NG ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPORTED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   THE ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE ALU-TRANSLATED ENTRY MUST HE TAKEN AS A WARNING THAT A ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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591
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  MW.
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FRAME 3.
FRAME 4.
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                                             FRAME 5
665D395735519D95 CRC64;
                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                                                          Usage by
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Query Match Best Local S Matches 31

Similarity

5.28;

Score 91.5; DE Pred. No. 3.4; 11; Mismatches

DH 1;

Length indels

37;

11,

Gaps

4

CHAIN SIGNAL

DOMA1 N

24 24 167

Phosphorylation: Glycoprotein: Signal.

23 POTENTIAL.

24 567 TGF-HETA RECEITOR TYPE 1

24 166 EXTRACELLULAR (POTENTIAL.

27 187 POTENTIAL.

ATP-binding:

TGE-BETA RECEPTOR TYPE 11 EXTRACELLULAR (POTENTIAL) POTENTIAL.

Transmembrane;

TRANSMEM

31;

Conservative

11;

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TGK2_KAT
PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
PROSITE: PS50011; PROTEIN_KINASE_ROM: 1.
Receptor: Transferase; Serine/Chreonine-protein kinase;
                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rat mesangial cell hypertrophy in response to transforming growth factor-beta 1.";
Kidney Int. 44:948-958(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATF: 1.
                                                                                      Pfam;
                                                                                                       InterPro: IPR000719; Eu._pkinase.
InterPro: IPR002290; Sci_thi_kin_actsite.
                                                                                                                                                                     HSSP; P00518; 1191K
                                                                                                                                                                                         PIR; JN0459; JN0459.
                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright.
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01+009+1994
                                                                                                                                                                                                                 EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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Mammalia: Entheria: Rodentia: Sciuroquathi: Muridae: Murihae: Kat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-A00-2001 (Red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F38438;
                                                                                                                                                   InterPro:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIANE-93221518; PubMed 8385453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_Tax11> 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOTHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + A PROTEIN + ADP + A PROSPHOPROFEIH SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIR. PIO STOLASMIC PIM: PROSPHORYLATED ON A SER/THR RESUDUE IN THE CYTOTASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: TYPE: 1/TYPE: 11 TGF-BETA AT COMPLEX AFTEK BINDING TGF-BETA AT SIGNAL TRANSDUCERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN. SIMILARITY: BELONGS TO THE SERZTHE FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGFH RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDDSFPNGVSLRPPGWSSVARSRLIAASTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARHHARLI PVPPVLTGFHYVAQAGLLLLLGSS-----DPPASASQSAGTTGVSH-----RAR 393
                                                                                   PF00069; pkinase;
                                                                                                                                                                                                                 $67770; AAH29352.2:
                                                                                                                                                                                                                                     L09653; AAA42237.1;
                                                                                                                                                 1PK000472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim - 43
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                                                                                                                                                   Activin_rec
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Binand C., B.
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Best Local
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     Yamada Y., Hassell J.R.;
"The complete sequence of perfecan, a basement membrane heparan sufface proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion
                                                                                                                                                                                                                                                                                  PGPM_MOUSE STANDARD; PRT; 3707 AA. (005793; 01-NOV-1995 (Rel. 32, Created) (01-NOV-1995 (Rel. 32, Last sequence update) (20-AUG-2001 (Rel. 40, Last annotation update) HASSEMENT MEMBRANE-SPECIFIC HEPARAN SHIPATE PROTEOCLYCAN
                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                              SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., MEDLINE-89034110; Pubmed-2972708;
                                                                                                                                                      Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki
Yamada Y., Hassell J.R.;
                                                                                                                                                                            MEDLINE+92078153; PubMed+1744087;
                                                                                                                                                                                      TISSUE-Melanoma;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                 J. Biol. Chem.
                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR003701: DNA_repair.
InterPro: IPR000934: Ser_thr_phosphuse
Piam: PFC25-9 :NV_repair.
                                                                                                                                                                                                                                                                 HSPG2
                                                                                                                                                                                                                                                                          PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrofase, Nucrease; Exonuclease; Complete proteomsEQUENCE 400 AA; 44713 MW; E8894089198C6D5B CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: AP002551: BAB33871.1; PIR: JS0349; JS0349. EcoGene; EG11094; sbcD.
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                                                                                                                                                                                                                                                      (Mouse).
  THIS PROTEIN IS
                                                                                                 266:22939-22947(1991).
                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         -VHLVTFSNGKLESVENLNVPVTQPMAVLKGDLASTTAQLEQWRD
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21.2%; Fred. No. 1
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  AN INTEGRAL COMPONENT OF BASEMENT
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Sciurognathi; Muridae; Murinae; Mus
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                                                                 SIGNAL
                                                                           Extracellular matrix; EGF-like domain.
                                                                                                           PROSTTE;
                                                                                                                      PROSITE;
                                                                                                                                                      PROSTTE;
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MEMBRANES. IT IS RESPONSIBLE FOR THE CIXED NEGATIVE ELECTROSTATIC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS
SUBSTRATE FOR CELLS.
                                                             SUCH AS LAMININ AND COLLAGEN TYPE IV
                                                             AND SERVES
                                                             Şς
                                                             AN ATTACHMENT
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DIMERS OR STELLATE STRUCTURES.
SUBCELLULAR LOCATION: EXTRACELLULAR

TISSUE SPECIFICITY: FOUND IN THE HASEMENT IN PERC. CONTAINS THREE HEPARAN SULFATE CHAINS AND G-LINKED OLIGOSACCHARIDES. MEMBRANIS AS WELL AS N-LINKIN

-!- SIMILARITY: CONTAINS 4 LDC-REALD FOR COMMAINS.
-!- SIMILARITY CONTAINS 10.5 LAMININ FROF-LIKE HOMAINS.
-!- SIMILARITY CONTAINS 15 LAMININ LOMALINS [V.
-!- SIMILARITY: CONTAINS 15 LAMININ C-LIKE C2-TYPE HOMAINS.
-!- SIMILARITY: CONTAINS 2 EACH-LIKE HOMAINS.
-!- SIMILARITY: CONTAINS 2 EACH-LIKE HOMAINS.
-!- SIMILARITY: CONTAINS 1 SEA HOMAIN.

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InterPro: 1PR002049: Laminin_EGE.
InterPro: 1PR001791; Laminin_G.
InterPro: 1PR000082: SEA.
Plam: PF00047: lq; 15.
Plam: PF00052: laminin_EGE: 8.
Plam: PF00053: laminin_EGE: 8.
Plam: PF00054; laminin_GC: 3.
Plam: PF00054; laminin_GC: 3.
Plam: PF00057: ldl_recept_a; 4.
Plam: PF00057: ldl_recept_a; 4. PRINTS: PRO0010: EGFFLOOD.

PRODOM: PD003031; Lamurin_B: 3
SMART: SM00180: EGF_Link: 7.
SMART: SM00001: EGF_Like: 6.
SMART: SM00001: EGF_Like: 6.
SMART: SM00281: Lamb: 3.
SMART: SM00282: Lamb: 3.
SMART: SM00282: Lamb: 3.
SMART: SM00292: Lamb: 3.
SMART: SM00292: EGF_L: 8.
SMART: SM00200: SEA: 11.
SMART: SM00200: SEA: 11.
SMART: SM00200: SEA: 11. InterPro; InterPro; InterPro: JPR001438; InterPro: JPR003006; JnterPro: JPR003598; InterPro; 1PR000561; EGF-1ike. InterPro; 1PR000742; EGF_2. InterPro; 1PR001438; EGF_11. Siqual: Basement membrane; Proteoglycan; Repeat: Glycoprotein; Heparan sulfate; Laminin EGF-like domain; Immunoqlobulin domai InterPro: MGD: MG1:96257; Hspq2. EMBL: M77174; AAA39911.1; J04054; AAA39899.1; J04055; AAA39912.1; ·. PS00022; EGF_1; 8. PS01J86; EGF_2; 5. PS01246; LAMININ_TYPE_EGF; PS01209; LDLRA_1; 4. PS50068; LDLRA_2, 4. PS50024; SEA; 1. JPK003598; JPK002J72; IPROOCO34; Laminin_B. 17.13 LDL_recept_A. 14_c2. Iq_MHC. =

182 182 183 180

194 234 359

LDL-RECEPTOR CLASS
LDL-RECEPTOR CLASS

>>> 3111

3707

POTENTIAL.

BASEMENT MEMBRANE-SPECIFIC HEPARAN

SULFATE PROTEOGLYCAN

CORE PROTEIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 ELKGGYIEKKDDEIVVNINIKVDIYNVEFNGDFRFFVNMEYOIVISVFNGNAYFRVITF- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 FASLTFEGTLGAPIIPRTSSKYFNFTFEDHKMVEALRVWASTHMSPSWTLLKLJDVQPMQ 16u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 YFDLTCQLLGKAEVDGASFTLKVWDGTRTPFPSWRVLIQDL-----VLEGDLSHHRLQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 -LICDVKKEETLSHKILRIKEDSCNKDKDLENKIKELLGLSYKYTIDOFNYKSVLARYRN 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 -- DVSFKKIDKENFKGLALFLK-----TQFLNKHTTLENFQLSKTSFLKTDVREV---
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Naom I.S., Morton S.J., Leach D.R.F., Lloyd R.G.;
"Molecular organization of sbcC, a gene that affects genetic
recombination and the viability of DNA palindromes in Escherichia
                                                              Science 273: 058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Protoobactor'us gamma subdicision, Entorobertor
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                               91.PF068862971776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.3;
; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EXONUCLEASE SBCD.
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                                                                                                                                                                                                                                                                                                                                                                                                 5.3%; Score 94.5; DI
19.8%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                           462 AA; 54433 MW;
                                                                                                                                                                                                                                                       EMBL; U67557; AAB99156.1; -. TIGR; MJ147; -.
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Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-015:HT KEMD 0509952; MEDGINE-21156231; PubMed-11258706; MEDGINE-21156231; PubMed-11258706; MEDGINE-21156231; PubMed-11258706; MEDGINE-21156231; PubMed-11258706; Medgine K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Oqasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinaqawa H.; Sanakawa G., Oqasawara O., Yasunaga T., Complete qenome sequence of enterohemorrhagic Escherichia coli oli57:H7 and qenomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *! FUNCTION: AFFECTS GENETIC RECOMBINATION AND THE VIABILITY OF DNA PALINDROMES IN E.COLL. SUCD MAY HAVE A NUCLEASE ACTIVITY THAT IS FUNCTIONALLY RELATED TO ONE OF THE NUCLEASE ACTIVITIES OF THE
                                                          SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
STRAIN-KIZ / MG1655;
BIACTINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Bilattner F.R., Plunkett G. III, Bloch C.A., Rose C.K., Mayhew G.F., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Dayls N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93146416; PubMed-1490631; Leach D.R.F., Lloyd R.G., Coulson A.F.; "The SbcCD protein of Escherichia coli is related to two putative uncleases in the UrrA superfamily of nucleotide-binding proteins."; Genetica 87:95-100(1992).
                                                                                                                                                                                                                                                                                                                Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed-11206551;
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Apodaca J., Anartharamun T.S., Lin J., Yen G., Schwartz D.C.,
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                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                     Nucleic Acids Res. 17:8033 8046(1989).
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MEDLINE-92138614; PubMed-1531222;
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SMART; SM004008; IGC2; 22.
SMART; SM00281; Lame; 3.
SMART; SM00282; Lame; 3.
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E; P$01186; EGF_2; 5.
E; P$01248; LAMININ_TYPE_EGF; 1
E; P$01209; LILIKA_1; 4.
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                                                                 NSDVDQLKKDLESANL/TANQHSDV1@GSEFDDSFPN-----GVSLRPP
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THAT_METLA STANDARD; PRT: 462 AA.

ID YHA7_METLA STANDARD; PRT: 462 AA.

AC Q58547;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 40, Last sequence update)

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                                                                                                                                                                                                                                                                                                                              NYEALPIIYKNGDIVRFHRLKIQVYKKETQGIT-----SSGFASLTFEGTLGAPIIPR 117
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Mammalia: Eutherla, Primales, Catarrhini, Hominidae, Homo.
NCDI_TaxiD=9606;
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                                                                                                                                                                                                                                            Ouery Match 5.8%; Score 102.5; DB 1; Length 560; Best Local Similarity 21.0%; Pred. No. 0.36;
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20-AUG-2001 (Rel. 40, Last annotation update)
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTECTINGONE
PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
                                                                                                                                            Hydrolase; Nuclease; Exonuclease; ATP-binding; DNA repair.
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                                                                                                                                                                                                                                                                                           46; Mismatches
or send an email to license@lsb-sib.ch).
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Kallunki P., Tryggvason K.;
                                                                        EMBL; AF158101; AAD42472.1; -.
                                                                                                                                                                                   560 AA; 63613 MW;
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01-0CT-1996 (Rel. 34, Created)
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                                    EMBL; X01804; CAA25945.1; -.
                                                                                                  EMBL; M10160; AAC05392.1; -. PIR; A04298; NCBPX6.
                                                                                                                                                                                                                                                                                       63; Conservative
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensed already.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. NAEL. ACAd. SCI. U.S.A. 90:10404-10408(1993).
PUNCTION: THIS PROTEIN IS AN INTEGRAL COMPONENT OF BASEMENT
MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTAFIC
CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILLYRATION
PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS
SUCH AS LAMININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of human heparan sulfate proteodlycan core protein, assignment of the gene (HSPG2) to 1p36.1-->p35 and identification ot a BamHI restriction fragment length polymorphism."; Genomics 11:389-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLENE-94052171; PubMed-8234307;
Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
"Structural characterization of the complete human perlecan gene and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                      "Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular expression, and mapping of the gene (HSPG2) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 4 LDL-RECREPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 32 IMMININDGLORALIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 SEA DOMAIN.
                                Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W., Yl H.F., Iozzo R.V.;
                                                                                                                                                                                                                                                                                                                                                                                   Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
Frygqvason K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACELLULAR, TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
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P00740; 11xA.
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InterPro; IPR00142; EGF_2.
InterPro; IPR001438; EGF_11.
InterPro; IPR00306; Iq_MIC.
InterPro; IPR003598; Iq_C2.
InterPro; IPR003172; LOL_recept_A.
MEDLINE-91365376; Pubmed-1679749;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE #92120660; Pubmed-1685141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND O'LINKED OLIGOSACCHARIDES.
                                                                                                                               cloning, cellular expression, an
short arm of human chromosome 1.
Genomics 10:673-680(1991),
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InterPro, 1PR002049; Laminin_EGF,
InterPro, 1PR001791; Laminin_G.
                                                                                                                                                                                                                                                                          SEQUENCE OF 892-1398 FROM N.A.
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EMBL; M85289; AAA52700.1;
EMBL; M64283; AAA52699.1;
EMBL; S76476; AA821121.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00052; laminin_B; 3. PF00053; laminin_EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21 FROM N.A.
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PF00047; iq; 22.
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Proc. Natl. Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M88282; AAA36662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a
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                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; 1PR003599;
                                                                                                                                                                                                                                                                                                                                                                lmmunoglobulin domain; Glycoprotein; Transmembrane; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFTER THE ACTIVATING STIMULUS.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
DATABASE: NAME-PROW: NOTE-CD guide CD96 entry:
DATABASE: NAME-PROW: NOTE-CD guide CD96 entry:
MWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd96.htm".
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SUBBUNT: HOMODIMER: DISULPIDE:LINKED.

SUBBULANTA LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EXPRESSED ON NORMAL T CELL LINES AND CLONES,
AND SOME TRANSPORMED T CELLS, BUT NO OTHER CHITURED CELL LINES
TESTED. IT IS EXPRESSED AT VERY LOW LEVELS ON ACTIVATED B CELLS.

DEVELOPMENTAL STACE: EXPRESSED AT VERY LOW LEVELS ON PEAKING 6 TO 9 DAYS

AND IS STRONGLY DI-REGULATED AFTER ACTIVATION, PEAKING 6 TO 9 DAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION AT A TIME AFTER T AND NK CELLS HAVE PENETRATED THE ENDOTHELIUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE AC
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FUNCTION: MAY BE INVOLVED IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: MAY BE INVOLVED IN ADHESTVE INTERACTIONS OF ACTIVATED AND NK CELLS BURING THE LATE PHASE OF THE IMBUNE RESPONSE, MAY
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1PR003006; 1g_MHC
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Query Match

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use by non-prolit institutions as long modified and this statement is not removed.

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13-AUC-1987 (Ref. 05, Created)
01-JAN-1990 (Ref. 13, Last seq
20-AUG-2001 (Ref. 40, Last ann
EXONUCLEASE SUBUNIT 2 (EC 3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genes 55, alpha gt, 47 and 46 of bacteriophage "4: the genomic organization as deduced by sequence analysis."; EMBO J. 4:257-264(1985).
                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hsu T., Karam J.;
Submitted (APR-1987) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases \lceil 3 \rceil
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Mesyanzhinov V., Ruger W., Stidham T.,
"Bacteriophage T4 genome analysis.":
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                                                                                                                    ween the Swiss institute of Bioinformatics and the European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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SIMILARITY: STRONG TO TS PROTEIN DI3 AND TO YEAST RADS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                            SUBCELEULAR LOCATION: NUCLEAR (PROBABLE).
SIMILARITY: BELONGS TO THE TELOMERE-BINDING PROTEIN ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 LTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHTHRLONLTIDTLVY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLFSCNYEALPIIYKNGDIVRFHRLKIQVYKKFTQGIT----SSGFASLTFEGTLGAPI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [P-----RTSSKYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 DTSKATWEUTVSRR----KFPRLYRGVTIKTRSVNIDSE-------TRRERGIAL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......IDEMYTPLSQARQEEGDFNVVGKVTQIVHRDYYTSDLRVK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DN-----HVHVARSLKVGSFLRTY-SLHTKLOSMNSENQTMLSLEFHLHGGTSYGRGTRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fang G., Gech T.R.;
"Molecular cloning of telomere-binding protein genes from Stylonychia
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 YIYTPLNOL--KGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQT-NVK-----LLC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 YEYTEIGSIEEENEASINFYAVVIDACEPYKVDEKKYMCYLKVIDTHHVVKEGDDNFAIV 78
Euplotes crassus has genes encoding telomere-binding proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDEGDDFTYRSYAYSGKQYNFDTQDQKLLKNTRAWNKSYFAKN------DV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  85;
                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 142.5; DB l; Length 460; 22.7%; Pred. No. 9.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alvoolata; Ciliophora; hypotrichs; Stichotrichida;
Oxytrichidae; Stylonychia.
NCBL_TaxID=5952;
                                                                                                                                                                                                                                                                                                                                  elomere; Multigene family.
EDIC141385A0B5FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  118;
            telomere-binding protein homologs.";
Nucleic Acids Res. 20:6621-6629(1992).
-!- FUNCTION: MAY BIND TELOMERIC T4G4 SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Greated)
01-APR-1993 (Rel. 25, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
TELOMERE-BINDING PROTEIN ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 AN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                            Nucleic Acids Res. 19:5515-5518(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92051290; PubMed-1945829;
                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 LPESN----SDVDQLKKDLES 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 APHSNIMTFVPFSRLAKSLDS 289
                                                                                                                                                                                                                                                                                                                                                                                                  Ouch y ...
Best Local Similaring
....rhes 73; Conservative
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.tsb-sib.ch/announce/
or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                        -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
-!- SUBCELLULAR LOCATION: NHCLEAR.
-!- MISCELLANEOUS: THE SEQUENCE OF STY56V IS SHOWN. STY56I DIFFERS IN ONLY ONE POSITION.
                                                                                                                                      -!- SIMILARITY: BELONGS TO THE TELOMERE-BINDING PROTEIN ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 LRAGEVVRERSATYDETSTOKKVILLSHYSNIVTEVSASKLAK - · EVKAKVTDDKSVEKA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
FUNCTION: MAY FUNCTION AS PROTECTIVE CAPPING OF THE SINGLE-STRANDED TELOMERIC OVERHANG. MAY ALSO PARTICIPATE IN TELOMERE LENGTH REGULATION DURING DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 STRYKYVELNKASIJISAEAQHFYGVVIDATFPYKTNOERYICSLKVVDPSLYLKSOKGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OL BASCIPPECTICAPTIPPET ----SSKYPNPTFIBDHKMVBALRVWASTHM----SPSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 ILKKIZDVOPMOYFDIJCOLIKKAEVDGASFLIJKVWDGTRTPFPSWRVIJQDLVLEGDLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 MESLEPHL, -----HGGTSYGRGTRVLPE----SNSDVDQLKKDLESANLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 ALKQDVSLSAVVLTEVDKKHAG ------LPTHSLQDLFHNADTD ---KETSSKDTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 HI-----REQUESTED------LLVYENHVHVARSEKVÖSFERLYSTHTKLQSMNSENQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butaleostomi,
Mammalia; Eutheria; Primates; Catarchini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ATNY LYTPLNQ - - LKGGT LVNVYGVVKFFKPPYLSKGTDYCSVVTLVD - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last aunotation update)
T-CELL SURFACE PROFEIN TACTILE PRECURSOR (CD96 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003415; Teto_bind_alpha.
Pr03307; Telo_bind_alpha. 1.
DNA-binding; Nuclear procein; Telomece; Multigene family VARIANT 429 429 1. (IN STYSEI).
SEQUENCE 493 AA; 56097 MW; B49002984363C5AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 135; DB 1; E. 21.1%; Pred. NO. 0.00048; ive 57; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 OTNVKLTCLLESGNYEALPTTYKNCDIVREGREGTOVYKKETO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 AA.
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                                                                                                                                                                                                                                                                                                                                                                             PIR; S22581; S22581.
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Matches 79; Conserv
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"Crystal structure of the Oxytricha
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                                                                                                                                                                                                                                                                                                                                                                             Horvath M.P., Schweiker V.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of a scrambled gene: the gene encoding alpha-telomere-binding protein in Oxytricha nova.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitcham J.L., Lynn A.J., "Analysis of a scrambled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92249771; PubMed=1577273;
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Oxytrichidae; Oxytricha
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s0-MAX-2000 (Ref. 39, Last annotation update)
TELUES... BINDING PROTEIN ALPHA SUBJUIT (TELOMERE-BINDING PROTEIN
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                            STRANDED TELOMERIC OVERHANG, MAY ALSO PARTICIPATE IN TELOMERE LENGTH REGULATION DURING DNA REPLICATION. BIND SPECIFICALLY TO THE TAGGE CONFAINING EXTENSION ON THE 3'STRAND AND PROTECT THIS REGION OF THE TELOMERE FROM NUCLEASE DIGESTION AND CHEMICAL MODIFICATION. SUBGULIT: HETERODIMER OF AN ALPHA AND A BETA SUBGULIT. SUBGELLANGUS: THE SEQUENCE OF THE A (OR ALANINE) VERSION IS SHOWN. THE SCOUENCE OF THE A (OR ALANINE) VERSION IS SHOWN. THE S (OR SERVINE) VERSION DIFFERS IN ONLY TWO DARTHY CANCELLY.
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01-JUN-1994 (Ref. 29, Last sequence update)
01-JUN-1994 (Ref. 29, Last annotation update)
TELOMERE-BINDING PROTEIN HOMOLOG.
SEQUENCE FROM N.A.
MEDLINE-93126105; PubMed-1480483;
Wang W., Skopp R., Scotield M., Price C.;
                                                                                                NCH1_Tax10~5936;
                                                                                                                               Euplotes
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Interfero: IPROUGHTS; Teto_bind_alpha.
Ptam; PF02307; Teto_bind_alpha; 1.
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Wed Apr 10 08:35:18 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein . protein search, using sw model

April 9, 2002, 17:11:12; Search time 22.97 Seconds (without alignments) 542.710 Million cell updates/sec Run on:

US-09-816-248-15 1776 1 MSLVPATNYIYTPLNQLKGG............LRPHYMSSVARSRLIAASTS 340 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	CONTRACTOR OF THE CONTRACTOR O	Control of the Control				_	P98160 homo sapien	U58547 met.hanococc	-	Q05793 mus musculu	P39188 homo sapien	P38438 rattus norv	P47297 mycoplasma	P15584 paramecium	014829 homo sapien	Ol 3290 schinosacch	e62 42 mus musculu	PO6786 saccharomyc	O9frx4 cucumis fiq	P46451 haomophilus	P39189 homo supien	P54787 saccharomyc	P27662 viral hemor	O64299 bacteriopha	P18480 saccharomyc	P11654 rattus norv	Q47862 erwinia her	P39195 homo sapien	P42224 homo sapien	P28824 xenopus lac	025165 helicobacte	P38427 saccharomyc	Ol3349 homo sanien
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	Qy 101FASLTFEGTLGAP11PRTSSKYFNFTTEDHKMVEALRVWASTHMSPSWTL 150 :: : :
	Oy 55 VKLTCLLFSGNYEALPIJYKNGDIVKPHRLKTOVYKKETOGITSSG
	Query Match 5.4%; Score 95.5; DH 2; Length 474; Best Local Similarity 21.0%; Fred. No. 3; Matches 66; Conservative 44; Mismatches 93; Indels III; Gaps 16;
	A;Gone: ATSP:F24J7.120 A;Map position: 4 A;Introns: 73/3: 102/3; 144/3: 205/2: 255/1 C:Superfamily: Arabidopsis thaliana hypothetical protein F24J7.161
	A;Accession: T06149 A;Accession: T06149 A;Molecule Cype: DNA A;Residucs: 1-474 <bev> A;Cross-reterences: EMBL:AL021768; GSPDB:GN00062; ATSP:F2437.120 A;Experimental source: cultivar Columbia; BAC clone F24J7 C;Genetics:</bev>
Mewes,	Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Bancroft, 1.; the Protein Sequence Database, April 1999 monter: Z15493
	RESULT 13 **T06149 hypothetical protein F24J7.120 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Apr-1999 **sequence_revision 30-Apr-1999 **Lext_change 15-Sep-2000 C:Date: T06149 C:Accession: T06149
	1007 DFMR
	328
	Cy 282 NSDVDQLKKD
	Qy 223 YDNHVHVARSLKVGSFLRIYSLHTK-LOSMNSENOTMLSLEFHLHGGTSYGRGLKVLPES 281
	Qy 163 DLTCQLLGKAEVDGASFILLKVWDGTRTDFPSWRVLLIQDLVLEGDLSHTHRLQNLTTDTLV 222 E: 11 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1
	CY 107 ECTLGAPITERTSSKYFNETTEDHKMVEALKVMASTHMSPSWTLLKICDVOPMOYE 162
	Gy 50 VDQTNVKLTCLLF****SGNYEALFLIJYKNGDIVRFHKLKIQVYKKETQGITSSGFASLTF 106 ::: : - - - - - - - - - - - - -
	Ouery Match 5.5%; Score 98; DK 2; Length 1198; Hest Local Similarity 21.4%; Pred. No. 7; Matches 65; Conservative 46; Mismatches 119; Indets 84; Gaps 15;
······	A:Gene: F2005.20 A:Map position: 1
	A:Accession: D46723 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-1198 <sto. a:cross-references:="" c:generics:<="" gb:ae005173:="" gspdh:gn00141="" nid:g2194131;="" p1dn:aab6;106.1;="" td=""></sto.>
_	A;Reference number: A86141; MUID:21016719

Oy 275 IRVLPESNSDVDOLKKDLESANI, 297 : : : : : :	OY 215 NLTIDILAYINHVHYAKSLKYGSPI.KTYSLHTKLOSHNSENOTMLSLEPHLHGGTSYGRG	OY 161 YFDLTCQLLGKAEVIGASFLLKVMDGTKTPFFSWRVLIQDLVLEGDLSHIHR	Oy 101 FASLTFEGTLGAPIIPRTSSKYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVOFMO	Oy 51 DOTNVKLTCLLFSGNYEALT/11YK	Qy 16 QLKGGT1VNPYGVVKFF-KPPYLSKGTDYGSVVTTV	Query Match 5.3%; Score 94.5; DR Hest Local Similarity 19.8%; Pred. Ro. 3.5; Matches 64; Conservative 58; Mismatches 1	Oy 184 WDGTRTPFIS
	NNSENOTMLSLIEPHLHGGTSYGRG 274 : ; ; ; ; ; ; LLGLSYKYIIDOPNYKSVLAEYRN 324	LIODLVLEGDLSHIHKLQ 214	RVWASTHMSPSWTLLKLCDVOPMQ 160 1: 27 SFNLLSFTDCKFRD 217	-NGD1VRFHRLK1QVYKKETQG1TSSG 100 	-KPPYLSKGTDYCSVVTIV 50 	DB 2: Length 462: 5; 5 120: indels 81: Gaps 14:	-WRYLIODLY

RESULT 15 JSO349 exonuclease (EC 3.1...) sheb - Escherichia coli C:Species: Escherichia coli

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N/Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote
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R:Heremans, A.; van der Schneren, B.; De Gock, B.; Paulsson, M.; Cassiman, J.J.; van der
J. Cell Biol. 109, 3199-3211, 1989
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                                        157 IVEDLLEVGTLAEMDKLNKALIRELNSQNQVLDVKKDSIIQQIKIYNDNVERQKKLTGDN 216
                       256 QTMLSLEFIILHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule Eype: mRNA
A;Residues; 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
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A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
A;Accession: A33625
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A;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>
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A;Accession: B33625
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                                                217 LTRLQ----
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C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G C;Keywords: chondroitin sulfate proteodlycan; dlyroprofein; heparan sulfate; transme F:1-21/Domain: signal sequence #status predicted <SIG> F:22-439/Product: perlecan #status predicted <MAT> F:22-193/Domain: I <DOMI>
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F;5571,7678hiding site: heparan sulfate (Ser) (covolent) #status predicted
F;89,554,7755,2121,3072,3105,3279,3780,3816,4068/Binding site: carbohydrate (Asn) (c
F;2995,3933,4179/Binding site: chondroltin sulfate (Ser) (covolent) #status predicte
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Nature 408, 816-820, 2000
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A.?Authors: Salzberg, S.L.; Schwartz, J.R.; Sinin, P.; Southwick, A.M.; Sun, H.; Tall ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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                                                                                                                 C:Species: Arabidopsis Lhaliana (mouse-dar cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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F.194-530/Domain: If CODM2>
F.194-234/Domain: If Cocceptor Liquad-binding repeat homology <LDI F.285-319/Domain: LDL receptor Liquad-binding repeat homology <LDI F.385-319/Domain: LDL receptor Liquad-binding repeat homology <LDI F.325-159/Domain: LDL receptor Liquad-binding repeat homology <LDI F.321-165/Domain: LDL receptor Liquad-binding repeat. homology <LDI F.31-167/CADmain: LDL receptor Liquad-binding repeat. homology <LDI F.31-167/CADmain: LIMININ - PAPE EGF-like homology <LEGS>
F.31-167/CADmain: LIMININ - PAPE EGF-like homology <LEGS>
F.363-1610/Domain: Luminin - PAPE EGF-like homology <LEGS>
F.364/CADmain: LA CADM4>
F.3007-2034/Domain: LA CADM4>
F.368/CADM3 - LONDM5>
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24.1%; Pred. No. 19;
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A:Title: Prediction of the coding sequences of unidal A:Reference number: Z14086; MUID:98290545 A:Accession: T00342 A:Status: Preliminary; translated from GH/EMBL/DDNJ A:Molecule type: mRNA A:Residues: 1-1044 <NAG>
                                                                                                         hypothetical protein KIAA0580 - human (tragment)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-JuJ-2000
C:Accession: T00342
R:Nagase: T:: Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.: Nomura, N
DNA kes. 5, 31-39, 1998
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T00342
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A:Reference number: Z19501
A;Acression: T22006
A:Status: preliminary: translated from GB/EMBL/EDBJ
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A:Introns: 42/3; 104/2; 160/3; 273/2; 3:7/2;
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                                                                                                                                                                                                                                                                                                            VPVDFRNEAFQ1FKKRVESVLEAVTDCDNF1EFQQKENVVQSE 239
                                                                                                                                                                                                                                                                                                                                                 LPES--NSDVDQLKKDLESA-----NLTANQHSDV1CQSE 310
                                                                                                                                                                                                                                                                                                                                                                                        DDHR1GIEKLNSGDFVALQNVHAASVGLTEMQVLHG---
                                                                                                                                                                                                                                                                                                                                                                                                                            DNHVHVARSLKVGSFLRIYSLH-----TKLQSMNSENQTMLSLEFHLHGGTSYGKGIRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDPRIGKAVEESGKEFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LGKA-EVDGASFLLKVWDGTRTPFPSWRVL1QDLVLEGDLSH1HRLQNLTID1LVY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFDVLAQVHSVVETKNGSWTLRVWRAQKFGPEASKEK----KEMNLFHVTENTFKCY1VI-126
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Pred. No. 0.29;
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                                                                                             of unidentified human
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                                                                                                                              Nomura, N.;
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C:Superfamily: phage T4 exonuclease 46
C:Keywords: exonuclease; hydrolase; nucleotide binding; P-loop
F:36-43/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: X01804; NID: q15229; PIDN: CAA25945.1; A; Note: the authors translated the initiation codon GUG for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 4, 257-264, 1985
A;Title: Genes 55, alpha-qt,
A;Relerence number: A91016; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: Nost Escherichia coli
C;Date: 17-Mar-1987 #sequence_revision
C;Accession: A04298; T10162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: phage T4
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A:Experimental source: brain: clone BJ0601
C:Geneties:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exonuclease 46 (EC + 1.11.-) chain
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           118
197 LIODLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQ-SMNSEN
                                                                                                                100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 TMAONCERTTATIVERCELLE THE HER TOTAL OF THE STATISTICAL OF THE STAT
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                                                                                                         ETTYNGTKLNESASSKDFOAEFEOLIG---MSYASFKOTVVLGTAGYTPFMGLSTPAKKK 156
                                                                                                                                                                                                                                                      KKCQL1 NSTNKKELLVE---LW-----
                                                                                                                                                                                                                                                                                                                       TSSKYFNFTTEDHKMVEALKVWASTHMSPSWTLLKLCDVQPMQY------F
                                                                                                                                                                                                                                                                                                                                                                                         NFKLNRVKYKNIMSVCQNGJDJQLDKVQKTLITGRNGGGKSTMLEAITF-GLFGKPFRDV 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 102.5; Dilarity 21.0%; Pred. No. 0.97; Conservative 46; Mismatches
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24.0%; Pred. No. 2.
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MUID:85257446
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184IIDEMYTPLSQARQEEGDFNVVGKVTQIVHRDYYTSDLRVK 224	R.Baynes, C. submitted bata Library, Novemb A.Reference number: 219634
	A:Accession: T22839 A:Status: preliminary; translated from GB/A:Molecule Lype: DNA A:Residues: 1-251 <wll></wll>
278 LPESNSDVDQLKKDLES 294 	A;Cross-references: EMBL:283110; PIDN A:Experimental source: clone F57C2 C;Cenetics: A;Cenetics: A;Map position: 2
v	A; Introns: 115/3; 198/2
ozona relomere-binding protein alpha chain - Stylonychia mytilus C;Species: Stylonychia mytilus C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999	Query Match 7.3%; Score 13 Best Local Similarity 25.7%; Pred. No Matches 52: Conservative 40: Misma
C:Accession: S.228B K.Pang, G.; Cech, T.R. Nucloic Acids Res. 19, 5515-5518, 1991 A:Tille: Molecular Confung Arth Maclomere-binding protein genes trom Stylonychia mytillis	OY 160 QYPDLTCQLLGKAEVDGASFLLKVWDC
A; Accession: S2281 A; Status: preliminary	QY 197 LIODLVLEGDLSHIHRĹONL/TIDILVYDNIVH'
	Db 85 RICKAIEENGKELLIEIDVYDDHRDG
A:Cross.references: EMBL:X61749; NID:q10194; PID:q578501 C:Conetics: A:Genetics: 27.23	QY 257 TMLSLEFHLH-GGTSYGRGIRVLPESNSDVI : Db 133 TEMQVLHGGGASYQRGITTVPVDFEHEAFG
C.Keywords: DNA binding; nucleus	QY 306 LCQSEP-DDSFPNGVSLR 322
Query Match 7.6%; Score 135; DB 2; Length 493; Best Local Similarity 21.1%; Prod. No. 0.0014; Matches 79; Conservative 57 Mismatches 148; Indole 90; Changes 15.	Db 190 VAENIVDEEPQEEALPRGVULR 211
GGT LVNVXGVVKFFK PLYT, SKGTDX CSVVT I VD	A46462 T-001 setting in the column of the co
YLKSOKGTG	cell activation antique Tactile · Numan (Species: Home sapiens (man) C.Date: 18-Jun-1993 #sequence revision 18
52 OTNVKLITCLLESGNYEALP119KNGD1VRPHRLKLOVYKKETOG1TS3G 100	C.Accession: A46462 R.Wang, P. L., O'Farrell, S., Clayborgo
90 DASDVATLVLYAKREFDLPITHRIGDTRVHRATLRLYNGOROFNANVFYNSSMALFSTD 149	A) imminol. 148, 2600-2608, 1992 A) Title: identification and molecular
FASLTFEGTLGAPIIPRTSSKYFNFTTEDHKMVEALRVWASTHMSPSWT	A; Accession: A46462; MUID:92218 A; Accession: A46462 A; Status: preliminary
150 KKSALQEIGGOEPASDITPFAFSGKNYTFFKSEAALLONIRKWAVOYFGOYNVISSDMFT 209	A; Molecule Eype: mRNA A; Residues: 1-569 - WAN.
150 LIKRINOPPROPENTECOLLIGERAEVDGASFILIKVWINGTREPPERRINULIODIJALEGDIJSH 209 	A: Gross-references: GB #M88282; NID:qB 48671; A: Note: sequence extracted from NGBL backbo
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262 LAAGEVVRLRSATYDETSTOKKVLLLASHYSNIVTFVSASKIJAK EVKAKVTDIKSVEKA 319	Query Match 6,1%; Score 109 [Rest, Local Similarity 20,7%; Pred, No.
HGGTSYGRGIRVLPBSNSDVDQLKKDLIBSANL;TA	OY 16 QEKGGTIVNVQQVKFFKPPVLSKGTDXG
300 NOHSDVICOSEPDD 313	DD 55 QMQMSKVTNK IDLIAVYHDOY GIPYCAYGR
368 TOFYITRVEPVD 379	Oy 62 -FSGNYEALPITYKNGDIVREHRLKIOVYKKET : : : :
RESULT 6 T122839 hypothetical protein F57C2.3 • Caenorhabditis alegans	

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5-Oct-1999 #text_change 15-Oct-1999
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40: 0.0014;
Matches 66; Indels 54; Gaps
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ADEW-NSNHTTELELNOTLEIPCPONSSS 169
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allehes 145; Indols ($\frac{1}{8}); Gaps
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bone (NCBIN:94434, NCBIP:94435)
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                                                                                   3/EMBL/DDBJ
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A: Residues: 1-446 < MAN.-
A: Cross reterences: EMBL:
C: Geneties:
A: Genetic code: SGC9
A: Introns: 9/3
C: Keywords: DNA binding:
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-495 <GRA>
A;Cross-references: GB:M68931; NJD:q159811; PJD:q159812
A;Accession: B41221
                                                                                                                                                                                                                                                          macronuclear alpha protein (alanine version) - (xytricha nova c:Species: Oxytricha nova c:Species: Oxytricha nova c:Species: Oxytricha nova c:Species: Oxytricha nova c:Date: 28-May-1992 **sequence_revision 28-May-1992 **text_change 02-Mar-2001 C;Accession: A41221; B41221 B41221 B41221; B41221 B4
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Nucleic Acids Res. 20, 6621-6629, 1992
A:Tille: Euplotes crassus has genes encoding telomere-binding A:Reference number: 835524; MUID:93126105
A:Accession: 835524
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C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C:Accession: S35524
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Pred, No. 2,3e-06;
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A:Genetic code: SGC9
A:Introns: 18/3; 377/3
C:Keywords: DNA binding: nuclous
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Nucleic Acids Res. 20, 6621-6629, 1992
A;Tille: Euplotes crassus has genes encoding telomere-binding
A;Reference number: 835524; M(1)):94126105
A;Accession: S35525
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C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-Dec-1999
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A; Residues: 1-460 <WAN>
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A:Molecule type: mRNA
A:Rosidnes: 1-310,/S:,312-455,7E7,457-495 -GR2-
A:Cross-reterences: GB:M68930; NID:q159813; PID
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                                                                                                                                                                                    9 YIYTPLNOL---KGGTTVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQT-NVK-----LTC
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                                                          ALQSRKFEDLP11QRCGD11RVHKAEYN-YKDDQHYFKLNMSYSSSWALFSADEEVAPEV
                       110------
                                                                                                 LLFSGNYEALFITYKNGDIVRFHKLKIQVYKKETQGIT----SSGFASLTFEGTIGAPI 114
                                                                                                                                             YEYTELGSI EEENEASINFYAVVIDACFPYKVDEKKYMCYLKVIDTTIINVKEGDDNFAIV
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23.5%;
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22.7%; Pred. No. 0.00029;
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Pred. No. 0.00015;
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April 9, 2002, 17:09:30 ; search time 38.59 Seconds (without alignments) 671.141 Million cell updates/sec
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1 MSLVPATNYIYTPLNQLKGG.............RPPGWSSVARSRLEAASTS 340
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES	0	T38425	835524	A41221	\$15525	S22581	T22839	A46462	T22006	T00 342	NCBPX6	A.38096	D96723	T06149	1364443	JS0349	D85535	S18252	G84306	F96763	E86692	886210	T32012	JN0459	F64205	S07744	871325	T21403	T30851	T18514
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RESULT

ALIGNMENTS

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9908-0145919. 9908-0145951. 9908-0146386. 9908-0146388.

9908-0147302. 9908-0147192. 9908-0147260. 9908-0147303. 9908-0147416.

99US-0146389 99US-0147038 99US-0147204

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27.JUL.1999
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23-JUL-1999;
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                                                                                           LVYDNHVHVARSLKVGSF-----LRIYSLH----TKLQSMNSENQTMLSLEFHLH 266
                                                                                                                                     131 KMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFILKVWDGTRTP 190
                                                                      53; Gaps
                         / Match 4.9%; Score 86.5; DB 21; Length 1002; Local Similarity 23.9%; Pred. No. 7.3; neg 45; Conservative 26; Mismatches 64; Indels 53;
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0145913 0145918 0145919 0145919 0145951 0146386 0146388	0145089. 0145192. 0145145. 0145218. 0145224. 0145276.	0144352. 0144884. 0144884. 0146314. 0145086. 0145088. 0145085.	0144085 0144086 0144325 0144331 0144332 0144333 0144333 0144333	0140695. 0140693. 0140891. 0141287. 0141287. 014285. 0142055. 0142390. 0142390. 0142390. 0142390. 0142390. 0142390. 0142390. 0142390.	0139455. 0139456. 0139456. 0139458. 0139459. 0139460. 0139462. 0139463. 0139750. 0139750. 0139899.	9908-0136782 9908-0136782 9908-0137222 9908-0137528 9908-0137528 9908-0137502 9908-0138640 9908-0138640 9908-0138647 9908-0138647 9908-0138647 9908-0138647 9908-0138647 9908-0138647 9908-0138647 9908-0138648
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25-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999; 26-OCT-1999; 28-OCT-1999;	21 - OCT - 1999; 21 - OCT - 1999; 22 - OCT - 1999; 22 - OCT - 1999; 22 - OCT - 1999; 25 - OCT - 1999;	14 - 0021 - 1999; 14 - 0021 - 1999; 18 - 0021 - 1999; 21 - 0021 - 1999; 21 - 0021 - 1999; 21 - 0021 - 1999; 21 - 0021 - 1999;	07-0CT 1999 08-0CT 1999 12-0CT 1999 13-0CT 1999 13-0CT 1999 13-0CT 1999 14-0CT 1999 14-0CT 1999	07 - SEP - 1999 10 - SEP - 1999 13 - SEP - 1999 15 - SEP - 1999 16 - SEP - 1999 22 - SEP - 1999 24 - SEP - 1999 26 - SEP - 1999 27 - SEP - 1999 28 - SEP - 1999 29 - SEP - 1999	1 / ARIC: 1999 16 ARIC: 1999 20 - ARIC: 1999 20 - ARIC: 1999 20 - ARIC: 1999 23 - ARIC: 1999 23 - ARIC: 1999 25 - ARIC: 1999 26 - ARIC: 1999 27 - ARIC: 1999 27 - ARIC: 1999 31 - ARIC: 1999 31 - ARIC: 1999 31 - ARIC: 1999	
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
1993 vigsppdielltvifnfilavhpptntyvchnptniytsihidgkligekvgslayirhs 2052
                                                                                    2053 ssgggatpspgflvispsattaappegtsssnivpqrmaaqmvrsrslp----afptylp 2108
                                                                                                                                                      2165 cemea-llqahasangvsrqsprfprarvdhkdvqteprsdddspydesyprrpdnlkgl 2223
                                            ------QDLVLEGDLSHIHRLQNLTIDILVYDNHVH 228
                                                                                                                              VARSLKVGSFLRIYSLHTKLQSM----NSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDV
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99US - 0123548.
99US - 0125788.
99US - 0126264.
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99US-0129845.
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990S - 0132407.
990S - 0132484.
990S - 0132485.
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99US-0135629.
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99US-0127462
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09-MAR-1999)
23-MAR-1999,
25-MAR-1999,
01-APR-1999,
06-APR-1999,
06-APR-1999,
16-APR-1999,
23-AAR-1999,
23-AAR-1999,
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14-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises the longer isoform of murine lysosomal trafficking regulator Lystl, a protein that regulates degranulation of lysosomes, late endosomes and acidic secretory granules primarily in leukocytes. Its sequence was deduced from a Lystl cDNA clone (AAT74199) that had been identified from a beige (bq) mutation critical region yeast artificial chromosome. Alternative splicing also yields a shorter isoform (see AAW23595) of Lystl. Homologous human sequences (see AAW23596 and AAW23597) have been continue Lystl and an are associated with Chediax Higashi syndrome (CHS). Murine Lystl and human Lystl polypoptides (see AAW23597) have been expressed in recombinant host cells for use in raising antibodies. Corpused in the development of therapeutic approaches to treatment of autolumnum diseases and certain types of rumours. The existence of an animal model of CHS with a similar quentic lesion will assist efforts to develop novel therapies for this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 CSVVTIVDQTNVKLTCLLFSGNYEALPIIYKNGDIVRFHRLKIQVYKKFTQGITSSGFAS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 88; DB 18; Lendth 3788;
18.8%; Pred. No. 43;
atlve 52; Mismatches 117; Indels 182; Gaps
                                                                                                                                                                   Lystl; mouse: lysosomal trafficking requiator;
Chediak-Higashi syndrome; CH syndrome; autoimmune disease; tumour;
vaccine; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian lysosomal trafficking regulators LYST1, Eyst1, EYST2 and Lyst2 - useful to diagnose Chediak-Hiyashi syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 -----THMSPSWTLLKLCDVQPMQYFDLTCQLLGK------THMSPSWTLLKLCDVQPMQYFDLTCQLLGK------A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kingsmore SF;
  AAW23594 standard; Protein; 3788 AA.
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96US-0011146.
96US-0033599.
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                                                                                 (first entry)
                                                                                                                              Murine Lystl long isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbosa-Alleyne MDFS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYFL ) UNIV FLORIDA.
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N-PSDB; AAT74199.
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                                                                                                                                                                                                                                                                                               WO9728262-A1
                                                                                                                                                                                                                                                       Mus musculus
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20-DEC-1996;
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                                          AAW23594;
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Best Local s
Matches 69
                                    18-JUL-2001
                                                                       AAB47250;
                                                                                                      AAB47250 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAHB1295 to AAHB1487 encode the Escherichia coli proteins given in AAG88239 to AAG88431, and AAHB1488 to AAHB1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prollieration of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or prollieration can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy. Expression of (1) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microorganism is capable of inhibiting proliferation of a microorganism. (1) have antibacterial and antibiotic activities, and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a purified or isolated nucleic acid sequences sequence (1) consisting essentially of one of the 93 nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids encoding proteins required for Escherichia coliferation, useful for screening for antimicrobial agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotides, which are used in the exemplification of the
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ilarity 21.2%; Pred. No. 0.29;
Conservative 38; Mismatches
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                              (first entry)
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                                                                                                      Protein;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targets to screening assays that identify agents a mitochondrial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide sequences which are then filtered and a report of the filtered set of polypeptide sequence information is then displayed. The computer system is useful for identifying recombinant C elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a desired polypeptide sequence. The computer searches the database based on a query formulated from the motif to obtain a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence shows a protein containing calmodulin/calcium binding motifs which was identified using the method of the invention. The method comprises a computer system for extracting information from biological sequence databases, which receives a motif that defines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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07-SEP-2000; 2000BS-0657253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p95.6/YN52 and other mitochondrial proteins involved in binding, transport or other regulation of intracellular calcium which provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulating intraced lular calcium ions and in drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Gaenorhabditis elegans mitochondrial calcium-binding protein, p95.6/YN52, identified by protein motif database searching, usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC85804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrial calcium-binding protein; p95.6/YN52; calcium; drug screening; sequence extraction; PP7; calcium binding motif.
                                                                                                                                                  180
295 nllhrvernkmksvlipptetnrdhdtdskh-nkvyvttnahgriktngspte 346
                                                                                                                                                                                                                                                                                                                                  120 SKYFNFTTED----HKMVEALK---VWASTHMSPSWTLLKLCDVQ-----PMQYFDLTC- 166
                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                             stf1sfmlenythihkeelelrnqsleseqdmrdrwdyvdsidvpdsyngprlqfpltct 119
                                                                         nlrygftkeilhkyklhqkrilqilevfyawlpiqtivdneilv----ihggisettdl
                                                                                                              SLKVC---SFLRIYSLHTK--LOSMNS-------ENOTMLSLEFHLHGGTSYGRGI
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RESULT 13 AAW23594

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769 meegnlpticlefkdsegregsvpavyl-ghidsfggsklqkmms-----ldesfalnli #22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli, identification, proliferation, microorganism, antimicrobial, antibacterial, antibiolic, acae therapy, diagnosis; bacterial growth inhibition.
                                                                                                                                                                                                                                                                                                      EGTLGA - - PTLPRTSSKYENFTFDHKMVEALRVWASTHMSPSW - - TLLKLCDVQPMOYF
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                                                                                                                                                                                                                                                                                                                                                              223 YDNHVHVARSLKVGSFLRIYSLHTK-LQSMNSENQTML, FFHLHGGTSYGRGIRVLPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%; Score 98; DB 21; Length 1198; 21.4%; Pred. No. 0.55;
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36; Mismatches
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9908-0161993.
9908-0162142.
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99US-0123548
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99US-0146386. 99US-0146388. 99US-0146389.	99US-0147038.	99US-0147302.	99US-014/192. 99US-0147260.	99US-0147303.	990S-0147415.	99US-0147935.	99US-0148171.	99US-0148341.	99US-0148565.	99US-0148684. 99US-0149368.	990S-0149175.	990S-0149426.	9905-0149723.	99US-0149929.	99US-0149930.	99US-0150566.	9905-0150884. 990S-0151065.	990S-0151066.	99US-0151080.	990S-0151303.	990S-0151930.	99US-0152363.	99US-0153070.	99US-0154018.	9905-0154039.	99US-0154779.	9908-0155486.	99US-0155659.	990S-0126596.	99US-0157117.	990S-0157865.	9905-0158029.	99US-0158232.	99US-0159291.	99US-0159294.	990S-0159335.	9908-0159330.	9908-0159331.	990S-0159638.	9908-0159584	990S-0160741.	990S-0160768.	990S-0160770.	99US-ULBUBL4.	990S-0160980.	99US-0160981.	99US-0160989.	990S-0161405.	99US-0161406.	990S-0161360.
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20-MAY-1999; 21-MAY-1999; 24-MAY-1999;	, 666	. 666	999;	:666	.666	, 660	:666	:666	666;	999;	399;	1666	:666	1666	. 666	399;	1666	. 666	399;	999;	. 666	666	1666	.666	999;	1666	1666	666	. 666	999;	999;	999;	666	7666	999;	666;	999;	1666	999;	999;	999;	999;	999;	1666	. 666	999;	666	. 666	999;	999;
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meegnlpficleikdsegregsvpavyl-qhidstqqsklqkmms-----ldestalnli 579
                                                  65;
                                                           Similarity
                                               5.5%; Score 98; DB 21; 1 itarity 21.4%; Pred. No. 0.38; Conservative 36; Mismatches 119;
                                                                                            9908-0161405.
9908-0161405.
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9908-0161361.
9908-0161920.
9908-0161922.
9908-0161993.
9908-0161993.
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99US-0148341,
99US-0148565,
99US-0148684,
                                              36;
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hybridisation assay; genetic
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9908-014226.
9908-014218.
9908-0134219.
9908-0134221.
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signal transduction pathway; metabolic pathway; mapping; gene expression control; promoter;

SEC 1D NO: 36956.

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    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
    232 SLKVGSFLRI-----YSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPES 281
                             Arabidopsis thaliana protein fragment SEQ ID NO: 36957
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Usurpin-gamma polypeptide

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                          AAB31889 standard; Protein; 4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides recombinant nucleic acid molecules encoding usurpin-alpha (lacking the first death effector domain (DED) or its prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are useful for in vitro and in vivo identification of usurpin-procaspase-8 interaction inhibitor. Usurpin is useful as moodulator of the sensitivity of cells to CD95(Fas/Apo-1) mediated appotensis. Modulation of apoptosis is useful for treating diseases like autoimmune diabetes, cancer and Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8 interaction are also useful for treating various diseases mediated by apoptosis. Usurpin provides an attractive model for modulating caspase activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be regulated at several levels in the presence of usurpin, conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant DNA molecules and polypeptides to treating apoptosis mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 11B; 69pp; English
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                                                                                                                                                                                                                                                                                                      216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance to Fas-ligand cell death. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                              in gene therapy (expression of sense or antisense sequences), they calso be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimen's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method of the invention. The specification describes a method which uses at least one polypoptide or polynucleotide sequence belonding to the perfecan, precursor of the retinol-binding plusma protein, precursor of the ganglioside GM2 activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple selecosis, using specipolypeptides or related nucleic acid or ligand .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's diseases, amyotrophic fateral selerosis, rheumatoid polyarthritis and lupus crythematosus, including use as vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurolodical disease; auto-immune disease; multiple selerosis; toxicity;
Alcheimer's disease; Parkinson's disease; amyotrophic lateral selerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents a human protein,
                                                                                                                                          sigmeas--itvtvtqtqanlaypaqstqpiricpsssqvaegqtldlncvvpaqshaq 2373
                                                                                                                                                                                                               tvaeqqtldlscvv-aqqahaqvtwykrqqslparhqvrqsrlyilqaspadaqqyvcra
                                                                                                                                                                                                                                                  TJVDQTNVKLTCLLFSGNYEALD LYKNGD1----VRFHRLK1-----
                                   TRTP----FPSWRVL1QDLVLEGDLSHTHRLQNLT1D1LVYDN-HVHV------AR
                                                                                                        ---HKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFLLKVWDG
                                                                                                                                                                               TQG1TSSGFASLTFEGTLGA------P1-1PRTSSKYFNFTTED---
                                                                     vtwhkrqqslpvrhqthqs----llilyqaspadsqeyvcrvlqssvpleasvlvtiepa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 138-152;
                                                                                                                                                                                                                                                                                                                                                                                 4393
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                                                        termination sequence.
                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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ilarity 98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tull-length cDMAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                          241 IYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTAN
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Otsuki T;
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11-JAN-2000; 2000JP-0118776.
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                                                                                                   KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL
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Otsuki T;
93.5%; score 1660; DB 22;
98.8%; Pred. No. 2.9e-171;
iive 2; Mismatches 2;
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27-AUG-1999; 99JP-0300253,
11-JAN-2000; 2000JP-0118776,
02-MAY-2000; 2000JP-0183767,
09-JUN-2000; 2000JP-0183767,
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Rest Local Similarity 98.8%;
Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sciencis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny. Inhibin activity, chemotactic/chemokinctic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
           Human Protein sequence SEQ
                                                              26-JUN-2001 (first entry)
                                                                                                                                                                             AAB92742 standard; Protein; 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in gene therapy. A composition containing a polypeptide of polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao
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Pred. No. 2.9e-171;
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sequence and an oligonucleolide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/4'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the discussion of the full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs.
                                    represent oligonucleotides, all of which are used of the present invention
                                                                         cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH1363.
                                                                                                                                                                                                                                                                                                            complementary strand of a polynucleotide which comprises a
                                                                                                                                                                                                                                                                                                                             of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                               oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
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02-MAY-2000;
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or diagnosis of the abnormality of the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
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2000JP-0183767.
2000JP-0241899.
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LKVWDGFRFFFFSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLR 240
                                   kyInfitedhkmvealrvwasthmspswillklcdvqpmqyIdltcqllqkaevdqasfl
                                                      KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL 180
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Length 634;

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April 9, 2002, 17:08:10 ; Search time 58.75 Seconds (without alignments) 428.679 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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13: /SID88/gcddala/panesseq/genesseqp/AA1992.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1992.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1992.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1993.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1995.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1995.DAT: 4 /SID88/gcddala/genesseq/genesseqp/AA1999.DAT: 4 /SID88/gcgdala/genesseq/genesseqp/AA1999.DAT: 5 /SID88/gcgdala/genesseq/genesseqp/AA1999.DAT: 5 /SID88/gcgdala/genesseq/genesseqp/AA2000.DAT: 5 /SID88/gcgdala/genesseq/genesseqp/AA2001.DAT: 5 /SID88/gcgdala/genesseq/genesseqp/AA2001.DAT: 6 /SID88/gcgdala/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq/genesseq/genesseq/genesseqp/AA1999.DAT: 6 /SID88/gcgdala/genesseq

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			Description	Human polypopt, ide	Human protein seem	Human protein sogn	Human protein sequ	Arabidopsis thalla	Visurpin-qamma polv	Amino acid seguenc	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Escherichia coli p
SUMMARTES			CD.	AAM40125	AAB92742	AAB93478	AAB95120	AAG58505	AAY67420	AAB31889	AAG30852	AAG30851	AAG30850 ·	AAG98362
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Human PP7. Homo s Murine Lystl long			Arabidopsis thalla	Arabidopsis thalta	Numan extracellula	Protein encoded by	Membrane-bound pro	Human extracellula	Human PRO698 (UNQ3	Human PRO698 prote	Bacillus subtilis	Human truncated St	84 kD ISGF-3alpha.	Human Stat84. Hom	Human STAT1-beta.	Human Stat1-beta p	91 kD tSGF-3alpha.	Human Stat91, Hom	Human STAT1-alpha.	Human Statl-alpha	Human signal trans	Human pancreatic c	Porphorymonas qinq	Human by protein a	Arabidopsis thalia	H. pylori GHPO 161	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalla	Eucalyptus grandis	Arabidopsis thalia	
AAB47250 AAW23594	AAG38741	AAG42603	AAG42602	AAG42601	AAY22201	AAY54368	AAY66646	AAE03653	AAB651.69	AAB50955	AAW98149	AAW62996	AAR4 1335	AAR72079	AAW03170	AAW62995	AAR41334	AAR72078	AAW03168	AAW62994	AAB19962	AAB54098	AAY34350	AAW31949	AAG23071	AAW98852	AAG31373 /	AAG23070	AAG23069 .	AAG31372	AAB25493	AAG31371	ALIGNMENTS
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All repeats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://tp.genome.washington.edu/RM/RepeatMasker:html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 177662; sum-of-contigs
Insert size: 145994; 25.7% error; ayarose-ip
Quality coverage: 11.36x in Q20 bases; sum-of-contigs Quality
coverage: 14.28x in Q20 bases; agarose-ip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CH10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 27, 2001 this sequence version replaced dil15020657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS1315A15 177762 bp DNA HTG 21-JUL-2001 HOME Sapiens chromosome 1 clone kP5-1115A15 map p36.11-36.01, *** SEQUENCING IN PROCRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dJ1115A15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: SC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177762)
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                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                        This record will be updated with the finished sequence as soon as it is available and the accession number wi be preserved.
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96648 177762: contig of 81115 bp in length
/map="p36.11-36.31"
/clone="RP5-1115A15"
                                                               /db_xre1-"taxon:9606"
/chromosome="1"
                                                                                                                /organism-"Homo sapiens"
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Best Local Similarity
Matches 134; Conserv
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3 (bases 1 to 166518)
Birren, H., Linton, L., Nusbaum, C., Landor, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Nastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colannelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
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                                                                                                                                                                                                        Karatas,A., Lehoczky,J., Lieu,G., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Molia,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Nifoff,M., O'Connot,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,K., Roberts,D., Roy,A., Severy,P., Stanqe-Thomann,N., Stojanevic,N., Stone,G., Subramanian,A., Testaye,S., Torruella-Miller,J., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
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Homo sapiens chromosome 17, clone RPJ1-138E18, complete sequence.
ACOUTA31
                                                                                                                                                          Submitted (29-APR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Mammalia; Eutheriä; Primates; Catarrhini; Hominidae; Homo.
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Complement (19538. 19811)
/rpt_family**AluJo"
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complement(18814. .18937)
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18975. .19175
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19492. .19537
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complement(25293, .25420)
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complement(25421, .25714)
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complement(25715, .25861)
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.25862, .26128 / rpt_canity" AluY" complement(26129, 26146) / rpt_canity" LlWC4" complement(26282, 26400) / rpt_canity" LlWC4" complement(26413, 26859) / rpt_canity" LlWC4" complement(26413, 26859) / rpt_canity" LlWC4" complement(26860, 27136) / rpt_canity" AluSq" complement(27147, 27435) /rpt_tumily="AluJo" complement(24725. .24759) /rpt_family="MLF2CB" 24760. .24788 /rpt_family-"Alusx"
22976
/rpt_family-"Alusx"
22977. 23962
/rpr_family-"(GGAA)n"
25997. 23694
/rpt_family-"(GGAA)n"
27697. 23694 repeat_region repeat_reqion repeat_region repeat_region repeat_reqion repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_reqion repeat_region repeat_reqion repeat_region repeat_region

Ouery Match 7.6%; Score 98; DB 9; Length 145122;
Best Local Similarity 69.0%; Pred. No. 1.1e-15;
Matches 149; Conservative 0; Mismatches 65; Indels 2; Gaps
7. 858 Ecuacidaaaaaqqatttaqaatciqcaaattiqaacaqccaatcaqaatqttat 917

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Matches 109; Conserv
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                                                                                                                                                                                 48045
                                                                                       7.6%; Score 98.2; DH 2; ilarity 85.8%; Pred. No. 9.4e-16; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"assembly_name:Contiq23"
81908. .89406
                                                                                                                                                                              /note="assembly_name:Contiq32"
46069 c 44860 g 49042 t
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64993. .72930
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                                                                                                                                                                                                             /note-"assembly_name:Contig31"
175718. .190737
                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig25"
99283, .111834
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45595. .51920
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36330, .40157
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31856. .36229
                                                                                                                                                                                                                                        /note="assembly_name:Contiq30"
162184. .175617
                                                                                                                                                                                                                                                                               /note="assembly_name:Contig29"
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135021, .145335
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40258. .45494
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23865. .27992
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18287. .23764
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13585. .18186
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126359. .134920
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SOURCE
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2 (bases 1
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DD 175524 ACTGCAGCCTCTACCTCCCGAGTTCAAGATCCTCCTGCCTCAGCCTCCCAAGTAGCTGGA 175465
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Submitted (12-MAR-2000) DOB Joint Genome Institute, Lawrence
Envermore National Laboratory, Livermore, CA 94550
Map and sequence oriented from centromere to q-telomere. HAC
C17-HISPC_360JII is overlapsed on the left by BC249609
(C17-HISPC_258N23) and overlaps BC321036 (C17-HSPC_444N24, AC005261)
on the right from bases 114293 to 145122 of this accession.
Additional chical 19 map and sequence information are available at
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1 (bases 1 to 145122)

Lamerdin, J.E. McCready, P.M. Skowronski, E., Viswanathan, V., Hurkhart-Schultz, K., Gordon, L., Dias, J., Kamirez, M., Stilwagen, S., Phan, H., Velasco, N., Dol., Regala, W., Terry, A., Brower, A., Carnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., avila, J., Liu, S., Andreise, T., Trankheim, M., Attix, C., Amico-Keller, G., Coelledd, J., Duarte, S., Lucas, S., Jurce, R., Andreise, T., Trankheim, M., Attix, C., Christensen, M., Carnes, C., Christensen, C., Christensen, M., Carnes, 
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Location/Qualifiers
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AC025588
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Lamerdin,J.E.
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complement(1187...1486
/rpt_famil...
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complement(2135. .2503)
/rpt_iamily~"LiM4"
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3017. .3126
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complement/77"
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/clone_lib-"CIT-HSPC"
/note-"LLNL_clone_name: BC288669"
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/db_xref="taxon:9606"
/chromosome="19"
/rpt_iamily-"FLAM_A"
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University School of Medicine, 4444 Forest Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 175089 TTTTGAGATGGAGTCTCGCTCTGTCGCCCAGGCTGGATGGCATGATCTTGGCTC 175030
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190737)
Materston, R. H.
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HOMO sapiens chromosome 11 clone RP11-706A13, WORKING DRAFT
SEQUENCE, 28 unordered pieces.
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On May 7, 2000 this sequence version replaced gi:7024180.
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83750: gap of unknown length
93283: contiq of 9533 bp in length
93883: gap of unknown length
102351: contig of 8968 bp in length
102451: gap of unknown length
129254: contig of 26803 bp in length
129354: gap of unknown length
176697: contig of 47343 bp in length
                                                                                                                                                                                                                                                                           2356 others
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Pred. No. 9.4e-16;
0; Mismatches 18; Indels
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Chemistry: Dye-terminator Big Dye: 22% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167225 bases at least 040
Consensus quality: 175317 bases at least 030
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                                                                                                                                                                                                                              /chromosome="11"
/clone="RP11-655D7"
41857 c 40829 g 44654 t
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                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                           Location/Qualifiers
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HTG: HTGS_PHASE1; HTGS_DRAFT
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                              7.6%;
Similarity 85.8%;
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* NOTE: This is a 'working draft' sequence. It currently consists of 28 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
            Insert size: 193000; aqarose-fp
Insert size: 188037; sum-of-contigs
Quality coverage: 3.04 in 020 bases; aqarose-fp
Quality coverage: 3.18 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 13434 bp in length
gap of unknown length
contig of 15020 bp in length.
                                                                                                                                                                                1325: contig of 1325 bp in length
                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                  1652 bp in length
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gap of unknown length
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of 10315 bp in length
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of 16648 bp in length
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gap of unknown length
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Consensus quality: 180039 bases at least 020
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1. .19073/ /organism~"Homo sapiens" /db_xref*"taxon:9606"

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Ouery Mutch 7.6%;
Best Local Similarity 76.6%;
Matches 134; Conservative
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Insert size: 196900; sum-of-conties
Ouality coverage: 10.78 in 020 bases; agarose-1p
Ouality coverage: 10.95 in 020 bases; sum-of-conties
                                                                                                                                                                                                                                                                                                      ACC21170 176697 bp DNA HTG 07-JUL-2
HOME Sapiens chromosome II clone KPII-655D7, WORKING DRAFT
SEQUENCE, 24 unordered pieces.
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176697)
Waterston, K.H.
                                      Unpublished
                                                                                      Waterston, R.H.
                                                                                                                                                                                      Homo sapiens
                                                               The sequence of Homo sapiens cloue
                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                             AC021170.4 CI:7235310
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                 (bases 1 to 176697)
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Pred. No. 7.3e-16;
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Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MC 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7024164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0655b07

NOTE: This is a 'working draft' sequence. It currently consists of 24 contiqs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contiqs are represented as runs of N, but the exact sizes of the daps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will

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Insert size: 174-99; sum-of-configs
Quality coverage: 3.57 in Q20 bases; agarcse-fp
Quality coverage: 4.02 in Q20 bases; sum-of-configs
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA HTG 12-JUN-2001
2 clone RP11-548P2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        945 tecaaatggagtetegettegteetecaggetggagtteagtggeaeggteteggeteat 1004
                                                                                                                                  885 aaatttgacagccaatcagcattcagatgttatctgtcaatcagaacctgacgacagctt 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO 63108, USA on May 17, 2001 this sequence version replaced gi:8570300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                  .;
                                                                 Length 74155;
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Insert size: 184246; sum-of-contigs
Quality coverage: 10.36 in Q20 bases; agarose-fp
Quality coverage: 9.90 in Q20 bases; sum-of-contigs
                                                                             73.4%; Pred. No. 3.9d-16; rative 0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; 69% Chemistry: Dyc-primer FT; 31% of reads Chemistry: Dyc-primer FT; 31% of reads Chemistry: Dyc-terminator Big Dyc; 69% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 175190 bases at least 030 Consensus quality: 184094 bases at least 020
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AC012511.6 GI:14140346
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN.
                                                             Score 99.6; DB 9;
Pred. No. 3.9d-16;
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Unpublished
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                            /rpt_family-"Alusx"
/rpt_family="AluJb"
40697, .41001
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Homo sapiens chromosome
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Waterston, R. H.
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                                                                 7.78;
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                                                                            Best Local Similarity 73.49
Matches 141; Conservative
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Mammalla, Eutheria, Primates, Calarrhini, Hominidae, Homo.
1 (bases 1 to 196900)
Waterston, R.H.
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Homo sapiens chromosome 2 clone RPI1-255N19, WORKING DRAFT
SEQUENCE, 1 unordered ploces.
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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29468: conting of 1996 bp in length
29568: app of unknown length
184446: contin of 154878 bp in length.
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
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10101. .29468
/note="assembly_name:Contig11"
29569. .18446
42294 c 42830 q 50771 t.
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                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     Location/Qualiflers
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Waterston, R.H.
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                            join(12813..12955,16901..16972,21399..21583,23281..2
37005..37082,44270..44346,45646..45747,46148..46258,
49729..49842,52001..52497)
                                                                 complement(11793...11925)
/TPt_family="MHR"
join(12813...12955,16901.
/gene-"Homo sapiens pyruvate dehydrogenase kinase
isoenzyme 3"
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10792. .11085
                                                                                                                                                                                                                /rpt_tamily="AT_rich" 10297, 10379
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/rpt_family="MER31A"
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9113. .9370
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10379. .10669
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//note="Region: N39012 yv22b03.sl Sources fetal liver spleen INFLS Homo sapiens cDNA clone 243437 3'*
5987. .6096
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7475. .7776
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3138. 3430
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/rpt_tamily-"L2"
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liver spicen INFLS Homo sapiens chan clone 243437 5."
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Complement/990*
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/map-"Xp22"
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/db_xref-"taxon:9606"
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38284. .38428
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47983. 30000
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37296. .37428
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35171. .35222
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complement(35295. .;
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25494, 25640
/rpt_family
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complement(17724, 1781 c)
/rpt_family-"AiuSx"
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20670. .20933
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/rpt_tamily~"MER2"
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/rpt_tamily-"Aluy"
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complement to
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9834. .9891
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2844. .2870
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/not=="maich to EST H23395 (NID:q892090) ym57q06.r1"
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/note="similar to Mus muscu
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             Sequence similarities were identified using Powerblast by Jinghui
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Submitted (02-JUL-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Pluza, H@uston, TX 77030, USA
On Jun 25, 1998 this sequence version replaced qi:3242666.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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Submitted (25-JUN-1998) Imman Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases I to 74155)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C. Direct Submission Direct Submission Submitted (02-MAY-1998) Molecular and Human Genetics, Baylor Submitted (02-MAY-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, US/3 (bases 1 to 74155)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C., Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Gancia, C., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Hornandez, J., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichtarge, O., Li, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Li, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Scherer, S. E., Shen, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, O., Williamson, A., Morley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
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RepeatMasker

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Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 14, 1999 this sequence version replaced gi:3213072.
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Submitted (14-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Manmalia, Eutheria, Frimates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-JAN-1999) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, 5 (bases 1 to 154959)
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Contact: sapiens@watson.wusti.edu
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This sequence was finished as follows unless otherwise noted:

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between nelghboring data submissions.

Center project name: H_DJ0907C10 Summary Statistics

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

and The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGAT Chromosome? Mapping Project (Fric D. Greet, Directol), John D. Merberson in the hepartment of Genetics (Washington University), and the Washington University Genome Sequence. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIRKGTMACHR7, seed mailto:eqreen@nhqri.nih.gov , or see http://qenome.wustl.edu/qsc MAPPING INFORMATION:

This clone was derived from human PAC library RPC1-5, prepared by refets de dons and coworkers at the Koswell Park Cancer Institute (http://bocpac.med.bullalo.edu) using the method described by toming or al., Nature Genetics 6:84-9 (1994). The library is Irc SOURCE INFORMATION:

The library is from

Actual start of this clone is at base position 1 of RP5-907C10, actual end is at 154959 of RP5-907C10. (http://www.qenomesystems.com) or Research Genetics, Inc. (http://www.resqen.com); or from Pieter de Jong. VECTOR: pCYPAC2 The clone may be obtained either from Genome Systems, NETCHBORING SEQUENCE INFORMATION: one male denor.

The sequence from 4689 to 5920 is from PCk product from PAC RPs-907C10 DNA.

FEATURES.

/organism "Homo sapiens" /db_xref "taxon:9606" /31. .752 /rpt_family="AT_rich" 1128. .1429 Location/Qualifiers 1. .154959 /map="7q31-3q32" /clone="kb5-907Cl0" /clone_lib="RPC1-5" 66, .259 /rpt_family="Alu" 1652. .1791 /rpt_family*"L1" 1810. .1936 /rpt_family*"L1" 1949. .2296 /rpt_family*"Alu" 2596. .2760 /rpt_family="L1" 2297. .2595 /rpt_lamily="L1" <2816. .25850 /rpt_family-"L1" /chromosome•"7 repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region Source dene

join(<2816, .2870,6849, .7005,8634, .8839,14398, .14533, 20470, .20558,22507, .22598,24455, .24560,25738, .25850) /qene="WUGSC:H_DJ0907C10.1" /gene= "WUGSC: H_D30907C10.1" 300

/trainslation-*GGSVSLYEVERCQOLSATILTDHQYLERTPLCATLKOKAPOQYR
TRAKLRSYRPRELFQSVKLHCPRCHLLOEVPHEGDLDIFDDGATKTPDVKLONTSLY
TRAKLRSYRPRELFQSVKLHCPRCHLLOFSPCHEGDLDIFDGGTLSEJCKLSNTSNY
TRAKLRSYRPRATYPRVNNGITHLDSNECLLIFBGGTLSEJCKLSNTRNYVYTPVR
SGHEDLELLDLSAPFLJOGTTHHYGCKOGSSLRSTQNLNSLVDKTSRIPSSVARALGT
VPLQYVFWTFTLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMLMFCPP /note-"supported by human ESTs H23395 (NID:q892090) and AA126363 (NID:q1687976), mouse ESTs W83982 (NID:q1344952) and AA717633 (NID:q2729907), and Genscan; H_DJ0907C10.1" /evidence-not_experimental /protein_id="AAD08852.1" /db_xref="G1:4176376" /codon_start+1

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Unpublished (2000)
2 (bases 1 to 1752)
Sugano,S., Suzuki,Y.,
                      Watanabe,K., Kumayai,A., Itakura,S., Yama:
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA, sequencing project
                                                                                                   oligo capping: fis (full insert sequence). Homo sapiens human small intestine cDNA to
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AK026234
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                                                                                   Homo sapiens
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
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Suzuki,Y.,
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Obayashi, M.,
                                                                          Craniata; Vertebrata;
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                                           Yamazaki,M., Tashiro,H.,
i,T., Shibahara,T., Tanak
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  Nishi,T.,
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Direct Submission

Submitted (29-AuG-2000) to the DDBJ/EMBL/GenBank databases. Sisubmitted (29-AuG-2000) to the DDBJ/EMBL/GenBank databases. Sisubmitted (19-Aug-2000) to the DDBJ/EMBL/GenBank databases. Sisubmitted (19-Aug-2000) to the DDBJ/EMBL/GenBank databases. Sisubmitted of Tokyo, Supano, Institute of Modical Science, University of Genome Structure Analysis, Human Genome Center; Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.)p, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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PUPETNISI VADDOLKKDI. JESAN TAVMIIRISVI YOOGSPEDIDSEPESOSVELI PEBECCOOLSA
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert.
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oligo capping; fis (full insert sequence).
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clone_lib:NT2RM2 clone:NT2RM2001544.
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Makamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and [wayanaqi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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sapiens cDNA FLJ10368 fis, cione NT2RM2001544
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/trains lation -"MSLVPATHY TYTPLHOLKGOT TVNVYGVVKFFKPPYLSKGTDYG
SVVT LVDQTHVKLTCLLFSGNYEALP I LYKNGD LVRFHRLK TQVYKKETQG LTSSGFA
SLTFEGTLGAP I LPRTSSKYFHFTTEDHKMVEALRVWASTHMSPSWTLLKLLGVQPWQ
                                                                                   /protein_id="BAA91568.1"
/db_xref="GI:7022355"
                                                                                                                                                                                                neuronal precursor cells
24. .1928
                                                                                                                                           /codon_start-1
                                                                                                                                                                                                                                                                                                    /cell_type-"teratocarcinoma"
/clone-"NT2RM2001544"
                                                                                                                                                                                                                                                                                                                                                       /cell_line-"NT2"
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                    /note-"unnamed
                                                                                                                                                                                                                                             /note-"cloning vector: pME18SFL3;
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DILVYDHIVHVARSLKVGSFLEI YSLHTKLQSMUSENGTWLSEFHLHGGTSYGRGIR
VLPESNISUDGLKKDLESSANLTANGISDVLCOS-SPEDDSSPSSGSVSLIYBVERGOOLSA
I ILTDHOYLERTPLAA LIKQKAPQQYR IRAKLRSYKPRRLFQSVKLHCPKCHLLQEVP
HEGDLDI I PQDCATKTPVVKLQNTSLYDSK LWTTKNQKGRKVAVHPVKNIG ILPLSNE
CILLI LEGGTLSEICKLSMKFNSV I PVRSGHEDLELLDLSAPFI, IQGT I HHYGCXOCSS
LKS I QNLMSLVDKTSM I PSSVAFALG I VPI-QYFVMTFTI, DDGTCVLEAY I MDSDKFF
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Local Similarity
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             TRACTETACGATAACCATGTTCATGTGGCAAGATCTCTGAAGGTTTGGAAAGCTTTCTTAGA
                                                                                                                         ttagtetaegataaeeatgtteatgtggeaagatetetgaaggttggaagetttettaga
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Caenorhabditis elegans
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WHEDLINE-20553141; Pubbed=11101850;

WICOLE S., Davoine C.S., Topaloglu H., Cattolico L., Barral D.,

Belghton P., Ben-Hamida C., Hammonda H., Cruaud C., White P.S.,

Belghton P., Ben-Hamida C., Hammonda H., Cruaud C., White P.S.,

Ramson D., Urtizberea J., Lehmann-Horn F., Weissenbach J.,

Ramson D., Urtizberea B.; A., Lehmann-Horn F., Weissenbach J.,

Ramson D., Urtizberea J., Lehmann-Horn F., Weissenbach J.,

Ramson D., Urtizberea J.,

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                                               Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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                                                                                                                               Genoscope:
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
HEPARAN SULFATE PROTEOGLYCAN PERLECAN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 102.5; 24.1%; Pred. No. 19;
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SM00181; EGF: 15.
SM000180; EGF_Lam: 12.
SM000019: EGF_Like; 7.
SM00409; IG: 22.
                            Homo sapiens (Human).
Eukaryota: Metazoa: Chordata;
Mammalia; Eutheria: Frimates:
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IG_like; 1.
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PROSITE; PS50068; LDLRA_2;
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SMART; SM00406;
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2351 VIWHKRGGSLPVRHQTHGS----LLRLYQASPADSGEYVCRVLGSSVPLEASVLVTIEPA 2406
                                                                                                                    2407 GSVPALGVIPTVRI -----ESSSSQVAEGQILDLNCLVAGQAHAQVTWHKRGGSLPAR 2459
                                                                                                                                                                                                                                                       2450 HQVHGSRLRLLOVTPADSGEYVCRVVGSSGTQEASVLVTIQQRLSGSHSQGVAYPVRIES 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 OYFDLICOLLGKAEVDGASFLLKVWDGTR------TPFPSWRVLIQDLV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLKVGSFLRJ.....YSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPES 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda: Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 LEGDLSHIHRLONLIIDILVYDNHVHVARSLKVGSFLRIYSLHTKLOSMNSENOTMLSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 FHLH-GGISYGRGIRVLPESNSDVD---QLKKDLESANLTANQHSDVICQSEPDDSFPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 QYFDLLAQVHSVVETMDGLWMLRVWRAQKFGPESIKERRERQLFHVTQFSFKRYIVPPNP
                                                                 187 TRIP----FPSWRVLIQDLVLEGDLSHIHRLONLTIDILVYDN-HVHV-----AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 215;
                                                                                                                                                                                                                                                                                                                                                                  SASLANGHILDLNCLVASQAPHIIIWYKRGGSLPSRHQIVGSKLKIP 2567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Indels
                                                                                                                                                                                                                                                                                                                         282 NSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPN-----GVSLRPP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McMurray A.A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; AL032671; CAA2177.2; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCI-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; ALOJZZZI; CARAZI777.2; JOINED.
EMBL; 281568; CAR76729.1; --
EMBL; ALOJZZZI; CAR76729.1; --
EMBL; ALOJZZZI; CAR76729.1; JOINED.
SEQUENCE 215 AA; 25209 MW; BE4975C081625390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (IrEMBLrel. 04, Created)
01-JUL-1997 (IrEMBLrel. 04, Last sequence update)
01-JUL-1997 (ITEMBLrel. 17, Last annotation update)
SIMILAR IO SYNECHOCYSTIS ANTIVIRAL PROTEIN.
F20PS.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 100.5; DE
25.9%; Pred. No. 0.43;
tive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- IEIDVY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNHVHVARSLKVGSFLRIYSLH-----TKLQSMNSENQIMLSLEFHLHGGTSYGRGIRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 DDHRIGIEKLNSGDFVALONVHAASVGLTEMOVLHG-------GGOAYNRGISK 195
                      133 IPVYPASAOVALLPPKOGESHKLLKEEHHOYVSYLYNVIDKYDVPDEAEYOORVKVSLNV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LGKA-EVDGASFLLKVWDGIRIPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVY 22?
                                                                  SPSWILLKLCDVQFMQYFDLTCQL-----LGKAEV-----DGASFLLKVWDGIRIP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mulson R., Ainscough M., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighting J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Persons J., Percy C., Rifken L., Roopra A., Saunders D., Shoxnkeen P.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Inherry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida: Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                      191 FPSWR---VLIODLVLEGDLSH--IHRLQNLTIDILVYDNHVHVAR--SLKVGSFLRIYS
                                                                                                                                                                     251 ASAARPADAYPEDNNPEAAQOHPWVGPYGKRTIQISCYDAHADFIREAGVSAGMWLSLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kershaw J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FATURE 366:32-38(1994).
EMBL: 281080; CAB03086.1; ..
SROUENCE 587 AA; 56502 MW; CF8A55F14188446F CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPES--NSDVDOLKKDLESA-----NLTANOHSDVICOSE 310
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02, Last sequence update)
13, Last annotation update)
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22.9%; Pred. No. v...
... 24; Mismatches
APII ------PRTSSKYFNFTTEDHKMVEAL-
                                                                                                                                                                                                                                                                                                                             587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  F39H2.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                      LHTK 247
                                                                                                                                                                                                                                         311 VQVK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kershaw J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 DLTCQLLGKAEVDGASFLLKVW---DGTRTPFPSWRVLTQDLVLEGDLSHIHRLQNLTID 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 LLEEIN-KKWCVLEGGFLSYYENDKSTTPNGTININEVICLAIHKEDFYLNTGPIF---I 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGILGAPIIPRISSKYFNFITEDHKMVEALRVWA---STHMSPSWTLLKLCDVQPMQYF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- QSMNSENQT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 IVDQINVKLICLL---FSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLT 105
                                                                                                                                                                                                           MEDLINE-98290545: Pubmed-9628581;
Nagase I., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                The complete sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

EMBL, AB011152; BAA25506.1;

Interpro: IPR000198; RhoGAP.

Interpro: IPR0001949; RhoGAP.

Interpro: IPR0001949; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 FE-----IYLPSERVFLFGAETS---QAQRKWTEAIAKHEVPLFA-ENLTEAD----Y
                                                                                                   Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 PIIVNSCIAFVIQYGLGCKYIYOKNGDPLHISELLESFKKDARSFKLRAGKH 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 MLSLEFHLHGGISYGRGIRVLPESNSD-----VDQLKKDLESANLTANQH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68E22A66DEAA53BD CRC64;
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Last sequence update)
Last annotation update)
                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 ILVYDNH-VHVARSLKVGSFLRIYSLHTKL------
Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.8%; Score 103; DB 24.0%; Pred. No. 2.3; tive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00169: PH; 4.
Pfam: PF00620: RhoGAP: 1.
Pfam: PF01412: ArfGap: 1.
PRINTS: PF00405: REVINTRACING.
PROSITE: PS50003: PH_DOMAIN: 3.
SMART: SM00105: ArfGap: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 AA; 119453 MW;
                                        01.NOV-1999 (TrEMBLEEL 12, 01.JUN-2001 (TrEMBLEEL 17, KIAA0580 PROTEIN (FRAGMENT).
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                         (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00233; PH; 3.
SMART; SM00324; RhoGAP; 1.
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Best Local Similarity 24.09
Matches 70; Conservative
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PRELIMINARY:
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=9505;
                                                                                                                                                                                                 IISSUE=BRAIN;
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09H3VS;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                             01-NOV-1999
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SECUENCE
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                                                                                      K1AA0580
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263 FHLH-GGISYGRGIRVLPESNSDVD---QLKKDLESANLTANQHSDVICQSEPDDSFPNG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2351 VIWHKRGGSLPVRHOTHGS----LLRLYQASPADSGEYVCRVLGSSVPLEASVLVTIEPA 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 QYFDLICQLLGKAEVDGASFLLKVWDGTR------TPFPSWRVLIQDLV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 LEGDLSHIHRLONLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Nematoda: Chromadorea; Rhabditida: Rhabditoidea; Rhabditidae; Peloderinae: Caenorhabditis.
NCBL_TaxID=5239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 QYFDLLAQVHSVVETHDGLWHLRVWRAQKFGPESIKERRERQLFHVTQFSFKRYIVPPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86. RIGKAIEEFGKEYL-IEINVYDEHRADLVSLNSGNFVAIONVHA-ASTPHREIOI----
                                                                                                          2407 GSVPALGVTPTVRI-----ESSSSOVAEGQTLDLNCLVAGQAHAOVTWHKRGGSLPAR
                                                                                                                                                          SLKVGSFLRI-----YSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPES
                                                                                                                                                                                                             2450 HOVHGSRLRLLQVTPADSGEYVCRVVGSSGTQEASVLVTIQQRLSGSHSQGVAYPVRIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 215;
                                                                                                                                                                                                                                                                                                    Indels
                                                        187 TRIP----FPSWRVLIODLVLEGDLSHIHRLQNLTIDILVYDN-HVHV----
                                                                                                                                                                                                                                                                  282 NSDVDOLKKDLESANLTANOHSDVICQSEPDDSFPN-----GVSLRPP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCI-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AL012671: CAA21777.2; -.
EMBL, 281568: CAA21777.2; -.
EMBL: 281568: CAA21777.2; JOINED.
EMBL: 281568: CAB75729.1; JOINED.
EMBL: AL012671: CAB75729.1; JOINED.
SEMBL: AL012671: CAB75729.1; JOINED.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO SYNECHOCYSTIS ANTIVIRAL PROTEIN.
F20P5.29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
3R5.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McMurray A.A.;
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09XWB2
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MEDLINE=20553141; PubMed=11101850;
MEDLINE=20553141; PubMed=11101850;
MEDLINE=20553141; PubMed=11101850;
MEDLINE=20553141; PubMed=11101850;
Medidine P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
Medidine D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
Mentadif F., Fondeline B.;
Ment
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                                                                                            Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4370;
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                                                             Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata: Eutele
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                              Genoscope:
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 19;
9; Mismatches 140;
           HEPARAN SULFATE PROTEOGLYCAN PERLECAN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I; UNKNOWN_1.
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Interpro; IPR000082; SEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR003596; Ig_v.
InterPro: IPR000034; Laminin_B.
InterPro: IPR002049; Laminin_EGF.
InterPro: IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Scor
24.1%; Preditive 39;
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Pfam: PF00053; laminin_EGF: 8.
Pfam: PF00054; laminin_G; 3.
Pfam: PF00057; ldl_recept_a; 4.
Pfam: PF01390; SEA: 1.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDLRECEPTOR.
Laminin_B; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003599; Ig.
IPR003598; Ig.c2.
IPR003600; Ig.like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00181; EGF; 15.
SM00180; EGF_Lam; 12.
SM00001; EGF_like; 7.
SM00409; IG; 22.
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IGv; 7.
IG_like; 1.
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SMART; SM00282; LamG; 3.
SMART; SM00192; LDLa; 4.
SMART; SM00200; SEA; 1.
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SMART; SM00406; I
SMART; SM00410; I
                                                                                                                                                  NCBI_TaxID=9505;
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263 FHLH:-GGTSYGRGIRVLPESNSDVD---QLKKDLESANLTANQHSDVICQSEPDDSFPNG 318
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                                                                                                                                                                                                   2460 HOVHGSRLRLLQVTPADSGEYVCRVVGSSGTQEASVLVTIQQRLSGSHSQGVAYPVRIES 2519
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2351 VIWHKRGGSLPVRHQIHGS----LLRLYQASPADSGEYVCRVLGSSVPLEASVLVTIEPA 2406
                                                                                                                                                     SLKVGSFLRI-----YSLHTKLOSMNSENQTMLSLËFHLHGGTSYGRGIRVLPES 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota: Metazoa; Namatoda; Chromadorea; Rhabditida: Rhabditoidea;
Rhabditidae; Peloderinae: Caenorhabditis.
NCBI_TAXID-5239;
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                                                      '187 TRIP----PPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDN-HVHV-----AR
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                                                                                                                                                                                                                                                         282 NSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPN----GVSLRPP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMurra; A.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AL032671; CAA21777.2; JOINED.
EMBL: 281568; CAA21777.2; JOINED.
EMBL: AL032671; CAB76729.1; JOINED.
EMBL: AL032671; CAB76729.1; JOINED.
SEQUENCE 215 AA: 25209 NW; BE4975C081625390 CRC64;
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01-101-1397 (TrEMBLrel. 04, Last sequence update)
01-JUL-1397 (TrEMBLrel. 17, Last annotation update)
SIMILAR 19 SYNECHOCYSTIS ANTIVIRAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (IrEMBLrel. 12, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
3R5.1 PROIEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              215 AA
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Best Local Similarity 25.9°
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                  MEDLINE-20553141; PubMed-11101850; MEDLINE-20553141; PubMed-11101850; Micole S., Davoine C.S., Topalogiu H., Cattolico L., Barral D.., Baighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S., Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J., Fortaine B.; Perlecan, the major proteoglycan of basement membranes, is altered in patients with Schwartz-Jampel syndrome (chondrodystrophic myctonia)." Nat. Genet. 26:480-483(2000).

11. Symilarity: 10 LOW DENSITY LIPOPPOIEIN (LDL) RECEPTCP CLASS A.
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                                                                                                    Euteleostomi;
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                                                                                                                                                                                                                                                      Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                    Craniata; Vertebrata; E
Catarrhini; Hominidae;
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tive 39; Mismatches 140;
                           HEPARAN SULFATE PROTEOGLYCAN PERLECAN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LDLRA) DOMAIN.

(LDLRA) DOMAIN.

EMBL: AL445795: CACIBS34 11: -
Interpro: IPPR000551: EGF-11ke.
Interpro: IPPR001559: Ig-2.
Interpro: IPPR001559: Ig-2.
Interpro: IPR001598: Ig-2.
Interpro: IPR001598: Ig-2.
Interpro: IPR001598: Ig-2.
Interpro: IPR001599: Laminin_B.
Interpro: IPR001591: Laminin_B.
Interpro: IPR001591: Laminin_B.
Interpro: IPR001791: Laminin_G.
IPR001
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SM00200; SEA; 1.
E; PS00022; EGF_1; UNKNOWN_1.
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SM00181; EGF; 15.
SM00180; EGF_Lam: 12.
SM00001; EGF_like; 7.
SM00409; IG; 22.
                                                                                              Eukaryota: Metazoa: Chordata:
Mammalia: Eutheria: Primates:
NCBI_TaxID=9505;
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SM00406; IGV; 7.
SM00410; IG_like: 1.
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PROSITE; PS50058; LDLRA_2;
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Matches 843
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Best Local Similarity 90.8 Matches 1178; Conservative
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/protein_id=Tabl4110.1"
/db_xref="GI:10434051"
/translation="MSLVPATNITYTPLNQLKGGTIVNYGVWFFKPPYLSKGTDYC
/translation="MSLVPATNITYTPLNQLKGGTIVNYGVWFFKPPYLSKGTDYC
SVYTIVDQTNYKLTCLLFGGNYEALPIIYNDGTNFPHRLKIQVYKETIGGTISSGFA
SLIFEGTLGAPIIPRTSSKYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVOPMQ
YFDLTGOLLGKAREVDGASFLIKVWDGTRTPPFSWRVLIQDLULEGDLSHIHRLONLTI
DILVYDNHVHVARSLKOGSFLRIYSLHTKOSMNSENQTMLSLEFHLHGGTSYGGIR
VLESNSDVDQLKRADLSAMITANQHSDVICQSEPDDSFPSGGSVLIFFVERCOOLSA
TILTDHQYLERTPLCAILKQRAPQOYRIRAKLRSYRPRLEGSYKLHCPKCHLLQEVP
HEGDLDIIFQDGATKTPDVKLQNTSLYBKRITTNRQKGRKVAVHFVNNGILPLSNE
CLLLIEGGTLESELCKLSNRFNYTPNTGIPPLLDGTGTHHYGGKQCSS
LRSIQNLNSLYDRTSWIPSSGHEDLELLDLSAPFLIGGTHHYGGKQCSS
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FDTTVAEDVI"
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/clone_lib="NT2RM2"
/note="cloning vector: pME18SFL3-mRNA from uninduced NT2 neuronal precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
1211 CGCATCCGAGCAAAATTGAGGTCATATAAGCCCAGAAGACTATTTCAGTCTGTTAAACTT 1270
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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518 fis, clone NT2RM2001805.
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Homo sapiens teratocarcinoma cell_line:NT2 cDNA
clone_lib:NT2RM2 clone:NT2RM2001805.
                                                                     /note="unnamed protein product"
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Query Match

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Pred. No. 7.5e-268;
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601672751F1 NIH_MGC_20 Homo
mRNA sequence.
BF027455
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EST.
Homo sapiens
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/lab_host="DH10B (phage-resistant)"
                                  GI:10735167
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ed. No. 1.8e-127;
Mismatches 6;
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                                                                     EST 10-00T-2000 cDNA clone IMAGE:3955573 5'
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1 (bases 1 to 920)

NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence start: 52
High quality sequence stop: 746.
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Tissue Procurement: ATCC/DCTD/DTP
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/tissue_type."melanotic melanoma"
/lab_host."DH10B (phaue-resistant)"
/note="Organ: skin: Vector: pOTB7; %
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/note-"Vector: pME1HSPL3; mKNA from uninduced NY2 neuronal
precursor cells"
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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamooto,J., Nakamura,Y., Nishikawa,T., Naqai,T., Sumuki,Y., Sudano,S., Sudano,S., Onpublished (2000)
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Ota,T., Wakamatsu,A., Ozawa,M., Ishii,Y., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Naqai,T., Suruai,Y., Suqano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: qenomics@hri.co.jp

HRZ human cDNA project; 5'- 6 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Gualifiers
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Klsarazu, Chiba 292-0812, Japan
Trei: 81-438-52-3951
Fax: 81-438-52-3952
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/clone_lib-"NT2KM2"
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Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1548-52-3951
Fax: 81-448-52-3951
Enaji: qenomics@dri.co.jp
HRJ human cDNA project; 57- k 3'-eud oue pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute; ol Medical Science, University of Tokyo, and
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Suqano,S. and
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Contact: Takao Isoqui,
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                            Song.H., Peng.Y., Gu.Y., Yang.Y., Gao.G., Xiao.H., Xu.X., Li,N., Qian.B., Liu.F., Qu.J., Gao.X., Cheng.Z., Xu.Z., Zeng.L., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M., Lu.G., Ye.M., Zhang.Q., Hu.R. and Chen.J.
Homo sapiens NPD library cDNA clones
Unpublished (2000)
Contact: Qinghua Žhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
                                                                         Eukaryota; Metazon; Chordata; ᢤraniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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/note="Vector: pME18SFLJ"
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Email: mbshl@ms.stn.sh.cn
This clone is available at
Shanghal.
Chinese National Human Geno
351 Guo Shoujing Road, Zhan
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                                     prime, mRNA
AL577671
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Location/Qualifiers
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/dev_stage="Adult"
/lab_host="SoLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI;
xhoI"
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/db_xref-"taxon:9606"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Fil, W.B., Gruber, C., Jessee, J. and Polayes, D.
Fil, Hentli chan libraries and normalization
Unpublished (2001)
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Vancart, Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Naqai,T., Suqano,S., and Isoqai,T., Yamamoto,J., Wakamura,Y., Naqai,T., Suqano,S., S. and Isoqai,T., Yamamoto,J., Wakamura,Y., Suzuki,Y., Ishii,S.,
Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura
V., Natuai,T., Suqano,S., Isoqai,T.)
Homo sapiens
Enkuryota: Metagoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genomicswhri.co.jp
HR) human cDNA project: 50 & 70 end one pass sequencing: Helix
Research Institute: CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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Pel: 81-4-84:52-9952
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/note="Vector: pME18SFL3"
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Genomies Laboratory
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Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 796)
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1 National Institutes of Health, Mammalian Gene Collection (MCC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11092 row: 1 column: 17 High quality sequence stop: 766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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RST25650 Athersys RAGE Library Homo sapiens cDNA,
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Mammalia: Entheria: Primates: Catarrhini: Hominidae: Homo.
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                                                                                                                                                                                                                                     High quality sequence stop: 514.
                                                                                                                                                                                                                                                                                                                           Contact: Scott J. Cain
Arhersys, inc.
                                                                                                                                                                                                                                                                                                                                                                  Activation of Gene Expression Nat. Biotechnol. 19 (5), 440 (2001)
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Fax: 216 361 9596
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                                                                                                                                                                                                                                                              Email: scain⊌athersγs.com
                                                                                                                                                                                                                                                                                                              3201 Carmedie Ave, Cleveland, OH
            /clone_lib-"Athersys RAGE Library"
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/cell_line-"See 'Creation of Genome-wide Protein Expression
/note-"See 'Creation of Genome-wide Protein Expression',
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next type indicated is HT1080, since a random activation
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2002, 08:33:16 : Search time 11.78 Seconds

(without alignments)
339.259 Million cell updates/sec

1 MSLVPATMYIYTPLNQLKGG......KKETQGIISSGFASLIFEGI ing
Scoring table: BLOSUM$2

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs. 35654827 residues

Ictal number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 0

Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:*

Database :

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its word from an original production in the European Bioinformatics Institute. There are no restrictions on its modeliad and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE TELOMERE-BINDING PROTEIN ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 NYIYIPLNQLK---GGIIVNVYGVVKFFKPPYLSKGID-YCSVVIIVDQINV-----K 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01.APR-1993 (Pel. 25, Created)
01.APR-1993 (Pel. 25, Last sequence update)
30.MAY-2000 (Pel. 39, Last annotation update)
TELOMBER-BINDING PROTEIN ALPHA SUBUNIT (TELOMBER-BINDING PROTEIN 55
RDA SUBUNIT) (TEBP ALPHA).
MAC-56A AND MAC-56K AND MAC-56S.
                                                                                                                                                                                                                                                                                                                                            Eukaryota: Alveolata; Ciliophora; hypotrichs: Euplotida: Euplotidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91126105: PubMed=1480483:
MEDLINE=91126105: PubMed=1480483:
MEDLINE=91126105: PubMed=1480483:
MEDLINE=91126105: PubMed=1480483:
MEDLINE=91126105: PubMed=1480483:
MEDLINE=91126105: PubMed=1480483:
MEDLINE=151045: PubMed=16001095: Lengine protein homologs: Lengine protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.4%; Score 104.5; DB 1; Length 445; 33.7%; Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR: S3524; S3554.
Interpro; IPR003415; Telo_bind_alpha.
Pfam: PF02307; Telo_bind_alpha: 1.
DNA_binding; Vuclear protein: Telomere; Multigene family: SEOUENCE 445 AA: 51544 MW; EF702FIE151990E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
     DASDYATLVLYAKPFEDLFIIHRIGDIIRVHRATLRLYHGGRO 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                       01-JUN-1994 (Pel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
TELOMERE-BINDING PROTEIN 51 KDA SUBUNII.
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                                                                                                                                                                                                                         Created)
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Best Local Similarity 33.73
Matches 33; Conservative
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NCBI_TaxID=5936;
                                                                                                                                                                                                                                                                                                                                    Euplotes crassus
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P29549;
                                                                                                                                                                      TEB_EUPCR
Q05184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL 39:303-344(1839D).

FUNCTION: MAY FUNCTION AS PROTECTIVE CAPPING OF THE SINGLE-STRANDED TELOMERIC OVERHANG. MAY ALSO PARTICIPATE IN TELOMERE LENGTH REGULATION DURING DAN REPLICATION. BIND SPECIFICALLY TO THE LENGTH REGULATION DURING DAN REPLICATION. BIND SPECIFICALLY TO THE THAT THE TELOMERE FROM NUCLEASE DIGESTION AND CHEMICAL MODIFICATION.

FOR THE TELOMERE FROM NUCLEASE DIGESTION AND CHEMICAL MODIFICATION.

FOR THE TELOMERE FROM NUCLEASE DIGESTION AND CHEMICAL MODIFICATION.

FOR THE TELOMERE FROM NUCLEAR.

FOR ALBANIATION.

FOR THE SOURCE OF THE A (OR ALANINE) VERSION IS SHOWN. THE S (OR SERINE) VERSION DIFFERS IN ONLY TWO POSITIONS, AND THE K VERSION IN ONLY ONE. THERE MAY BE OTHER VERSIONS IN ADDITION TO THE S. A. AND K VERSIONS.

FOR THE TELOMERE S. A. AND K VERSIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of the Oxytricha nova telomere end binding protein "Crystad with single strand DNA.": ceplexed with single strand DNA.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 YGVVKFFKPPYLSKGIDYCSVVTIVDQT-----NVKLTCLLFSGNYEALPIIY 73
                                                                                                                                     SECUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92035001: PubMed=1840510;
Gray J.I., Celander D.W., Price C.M., Cech T.R.;
"Cloning and expression of genes for the Oxytricha telomere-binding protein: specific subunit interactions in the telomeric complex.";
protein: $Pecific subunit interactions in the telomeric complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
Eukaryota: Alreolata: Ciliophora: hypotrichs: Stichotrichida:
Oxytrichidae: Oxytricha.
NCBL_TaxID~5945:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-PAY CRYSIALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-99091054: PubMed-9875850:
Horrath M.P., Schweiker V.L., Bevilacqua J.M., Ruggles J.A., Schultz S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.18; Score 97; DR 1; Length 495; 30.98; Pred. No. 0.004; ive 14; Mismatches 30; Indels
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PIR: B41221: B41221.
PDB: 101C: 12-APR-99.
InterPro: 1PK003415: Telo_bind_alpha.
InterPro: Telo_bind_alpha: 1.
PMA-binding: Nuclear protein: Telomere: Multigene family:
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A -> S (IN S VERSION).
D -> E (IN S VERSION).
; 9FD3CD40E623359B CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-52249771; PubMed-1577273;
Mitcham J.L., Lynn A.J., Prescott D.M.;
"Analysis of a scrambled gene: the gene encoding
alpha-telomere-binding protein in Oxytricha nova.
Genes Dev. 6:788-800(1992).
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455 D
55082 MW;
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EMBL: M68930; AAA29399.1; -.
EMBL: X59724; CAA42409.1; -.
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495 AA;
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25: Conserv
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Euplotes

I EBH_EUPCR

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IISSUE=Small intestine:
MEDLINE=95058376; PubMed=7968686;
Wada A., Hirayama I., Kitao S., Fujisawa J.-I., Hidaka
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                                                                                                                                           Immunol. 38:535-541(1994).
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HSSP: Q02846: lAWL.
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454
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1073
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Microbiol. Immunol.
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CARROHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-FPOI entry is copyright. It is produced through a cullaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and to commercial entities requires a license agreement (See http://www.ish-sil.ch/announce/or send an email to license@ish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                19 YEYTEIGSIEEENEASINFYAVVIDACFPYKVDEKKYMCYLKVIDIIHNVKEGDDWLAIV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIYTPLNQL--KGGIIVNWYGVVKFFKPPYLSKGIDYCSVVIIVDOI-NVK-----1C 59
                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Ciliophora; hypotrichs; Euplotida; Euplotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enteleost/ Ti:
Sus.
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20-AUG-2001 (Rel. 49, Last annotation update)
HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUCYZC OR GUCZC)
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 90; DB 1; Length 450; 31.4%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR: $35525; $35525.
InterPro: IPR003415; Telo_bind_alpha.
Pfam: PF02307; Telo_bind_alpha; 1.
DNA binding: Nuclear protein: Telomere: Multigene family.
SEQUENCE 460 AA: 53360 MW; EDIC141385A0B5FE CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata: Vertebrata;
Cetartiodactyla; Suina: Suidae;
                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq:
01-JUN-1994 (Rel. 29, Last anno
  : |||:| || :::| : |
115 RAGDIIRVHRAILFLYNGQRQ 135
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Best Local Similarity 31.4°
Matches 33; Conservative
                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                             Euplotes crassus
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5936;
                                                                                                                            TEBH_EUPCR
Q06183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR FOR THE E.COLI HEAT-STABLE ENTEROTOXIN (E.COLI ENTEROTOXIN HARKEDLY STIMULATES THE ACCUMULATION OF CGMP IN MARMALIAN CELLS EXPRESSING GC-C). ALSO ACTIVATED BY THE ENDOGENOUS PEPTIDE GUANYLIN (BY SIMILARITY).

-!- CATIVATITY: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SETTING STATES S
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PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM: 1.

PROCEDITE; PS50011; PROTEIN_KINASE_DOM: 1.

PROCEDITE; PS50011; PROTEIN_KINASE_DOM: 1.

POTENTIAL.

1.23
"pig intestinal membrane-bound receptor (quanylyl cyclase) for heatstable enterot" vin: cDNA cloning, functional expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LROIKGGIIV---NVYGVVKFFKPPYLSKGT---DYCS---VVTIVDQTRVKLTCLLFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAT-STABLE ENTEROTOXIN RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 72.5; DB 1; Length 1073; 29.5%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYEAL ---- PIIYKNGDIVRFHRLKIQVYKKETQGITSSGFA----SLTFEG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARIIY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE-LIKE.
GUANYLATE CYCLASE.
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HSEP_PIG

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NCP1_Tax1D=63363;
                                                                                                                 aeolicus.
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COFA_BOVIN
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                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for cornercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 SEQUENCE FROM N.A.

Yamada T., Ohki S.T., Osaki T.;

Yamada T., Ohki S.T., Osaki T.;

Yamada T., Ohki S.T., Osaki T.;

*Clonling and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";

Plant Biotechnol. 17:337-340(2000).

*! CARALVITG ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOXE AI ONE
SPECIFIC ADENOSINE ON THE 28E RPNA.

SPECIFIC ADENOSINE ON THE 28E RPNA.

*SPECIFIC ADENOSINE ON THE 28E RPNA.

PROTEINS: BELCNGS TO TYPE 1 RIP.
                                              20-AUG-2001 (Rel. 40. Created)
20-AUG-2001 (Pel. 40. Last sedence update)
20-AUG-2001 (Rel. 40. Last annotation update)
PUTATIVE RIBOSOME-INACIIVATING PROTEIN PRECURSOR (RRNA N-GLYCCEIDASE)
(EC. 3.2.2.22).
                                                                                                                                      Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta: eudicotyledons; core eudicots; Posidae;
eurosids I: Cucurbitales; Cucurbitaceae; Cucumis.
NCBL_TAXID-131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LVPATN----YIYIPLNOLKGGIIVNVYGVVKFFKPPYLSKGIDYGSVVTIVDQINVELT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
N.LINKED (GLCNAC. . . ) (POTENTIAL.
N.LINKED (GLCNAC. . . ) (POTENTIAL.)
N.LINKED (GLCNAC. . . ) (POTENTIAL.)
N.LINKED (GLCNAC. . . ) (POTENTIAL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 SKFVFOGTKSITLPYSGNYOKLO------SVAPKEPDS-FLGFMA: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Antiviral: Protein synthesis inhibitor; Hydrolase; Toxin; Sig: 31.
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ا -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------CLLFSGNYEALPIJYKNGDIVRFHRLKIOVYKKETGGITSSGFAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%; Score 70.5; DB 1; Length 285; ilarity 25.6%; Pred. No. 1.7; Conservative 13; Mismatches 37; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4EFD4966E604DA41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE III ALPHA SUBUNII (EC 2.7.7.7),
DNAE OR AQL1008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria: Aquificales: Aquificaceae; Aquifex
                                    285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB045560; BAB19677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31771 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001574; RIP. Pfam; PF00161; RIP; 1.
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
103
110
252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
103
110
252
286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 30; Conserv
                                                                                                                         Cucumis figarei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP3A_AQUAE
057125;
                                    RIPL CUCFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                       RIP1_CUCFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBUNIT: CONTAINS A CORÉ (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAI ASSOCIATES WITH A TAM SUBUNIT WHICH ALLOW THE CORE DIMETIZATION TO FORM THE POLITI' COMPLEX, POLITI' ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELIA, DELIA', PSI, AND CHI) AND WITH THE BETTA CHAIN (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: CYTOPLEANIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PAINY-----IYTPLNOLK-----GGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQ 52
                                                                                                    ď
                                                                                                                                                                                                                                  Nature 392:353-358(1998).

-: PUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME PESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE ALFAH CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).

-: CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Everyotas Melazoa: Chordata: Craniata: Vertebrata: Buteleostomi:
Marralia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovoldea:
Bovidae: Bovinae: Bos.
                                                               Deckert G. Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Grahan D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Fe). 35, Created)
01-NOV-1997 (Fe). 35, Last sequence update)
01-NOV-1997 (Fe). 40, Last annotation update)
020-MG-2001 (Ee). 40, Last annotation update)
030-MG-2001 (ALPHA SUBUNI) (ALPHA-COAT PROTEIN) (ALPHA-COP) (HEDCOP)
(HED-COP) (CONTAINS: XENIN (XENOPSIN-RELATED PEPTIDE); PROXENIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 69.5; DB 1; Length 1161; 29.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 24, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1161 AA: 133207 MW; 619F7436E1262BD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1224 AA.
                             MEDLINE-98195555; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AE000718: AAC07087.1; -. InterPro: IPR003141; PHF_N. InterPro: IPR002309: tRNA-synt_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coery Match
Best Local Similarity
Matches 22: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
SECHENCE 1161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCPA_BOVIN
Q27954;
SIPAIN=VF5
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5 gt 12

87 AA.

PRT;

STAMPARD;

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01-NYV-1997 (Rel. 35, Created)
01-NYV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Fel. 40, Last annotation update)
ARGINYL-TRNA SYMIHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Bacterial genetics by flow cytometry: rapid isolation of Salmonella typhimurium acid-inducible promoters by differential fluorescence induction.";
                                                                                                                                                                                                                                                                    Salmonella typhim wium.
Pacteria: Protechecteria: damma subdivision; Enterobacteriaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEAIN-SL1344:
MEDLINE~97084577: PubMed=8930920:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valdivia R.H., Falkow S.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCB1_Tax1D=602;
                                                                                                                                                                                                   (FPAGMENT).
                                                                                                                                                                                                                                                                                                                                           Salmonella.
SYR_SAL1Y
P74871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRP STESU
   STANDAR OCCORDED ON THE STANDAR OF STANDAR O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its sie, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                            Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

10 DILYSINE MOJIES AND REVERSIBLY ASSOCIATES WITH GCLGI NOH-
CLATHRIN-COATED VESICLES. WHICH FURTHED MEDIATE PHOSYNTHEILC
CLATHRIN-COATED VESICLES. WHICH FURTHED MEDIATE PROSYNTHEILC
CLATHRIN-COATED VESICLES. WHICH FURTHED MODIAGE FROM GOLGI
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
NETWORK. CANDONER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CAN ONLY BE RECENTIED BY MEMBRANES ASSOCIATED TO ADD-RIBOSYLATION
FACTORS (ARFS), WHICH ARE STALL GTP-BINDIN; PROTEINS: THE COMPLEX
ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY. AS WELL AS THE
PROCESSING, ACTIVITY, AND ENDOCYTIC PECYCLING OF LDL RECEPTORS (BY
STHALDARIY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
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SUBUNIT: OLIGOMEPIC COMPLEX THAI CONSISTS OF AT LEAST THE ALPHA, BETA, GAMMA, DELTA, EPSILON AND ZELS SUBUNITS.
SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OF POLYMERIZED ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE VESICLES/BUDS OPIGINATING FROM IT (BY SIMILARITY). XENIN IS SECRETED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 YIYIPLMQLKGGILVHVYGVVKFFK-PPYLS--KGID-YC------SVVIIVPQIHVKL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X95768; CAA55543.1; -.
InterPro; IPR001580: WD40.
InterPro; IPR001580: WD40.
PRINTS; PR00320: GFFOTELNBRPT.
SMART: SM00320: WD40: 6.
PROSITE: PS00678: WD_EEPEATS_1; 1.
PROSITE: FS0029: WD_EEPEATS_2; 6.
PPOSITE: FS0029: WD_EEPEATS_2; 6.
PPOSITE: FS0029: WD_EEPEATS_2; 6.
PFOSITE: FS0029: WD_EEPEATS_2; 6.
PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C9350BF2AC00683D CRC54:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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WD 2.
WD 3.
WD 4.
WD 5.
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nes 23; Conservative
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91
133
203
247
1224 AA:
                                          SEQUENCE FROM N.A.
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Rest Local Si
Matches 23;
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SEQUENCE
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PEPTIDE
                                                                              Wieland
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                                                                                                                                                                                                                                                                                                                                                                            -:- SUBBNIT: MOROMER.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptonorcus suis.
Bacteria: Firmicules: Bacillus/Glostridium group: Streptococcaceae:
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01-001-1993 (Fol. 27, Last sequence update)
01-001-1994 (Pol. 30, Last annotation update)
MUSAMIDASE PELEASED PROTEIN PRECURSOR (136 KDA SURFACE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM M.A.
STRAIN-SEROINE 2 / D282;
MEDLINE 92257650; PubMed=1587602;
Smith H.E., Vecht U., Gielkens A.L., Smits M.A.;
"Cloning and nucleotide sequence of the gene encoding the 175-kilodalton surface protein (muramidase-released protein)
#CI. Microbiol. 22:267-378(1995).
-!- CATALYTIC ACTIVITY: AIP + L-ARGININE + TRNA(ARG) = AMP
PYROPHOSPHAIE + L-ARGINYL-TRNA(ARG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 57; DB 1; Length 87; llarity 45.2%; Pred. No. 1.1; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LFSGNYEALFILYKNGDIVRFHRLK-IOVYKKETQ-GIISSG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 LFSGFYEHCPILSAENDAVRNSRLKLVQLTAKILKLGLDTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT: 1255 AA.
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Post Local Similarity
Matches 19: Conserv
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P32653:
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PESULT 9

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SIEAIN-972;
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Q9ZM57:
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ROVE_HELPJ
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            NOTE THAN THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                     This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL cutstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and ic: commercial entities requires a license agreement (See http://www.isb-sih.nh/announce/or send an email to licensefisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2' : Gaps
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                                                                     -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, CELI WALL.
-1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PP. FINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VP34_SCHPO STANDAED: PPT; 801 AA.
VP34_SCHPO STANDAED:
P50520: 02P3W2: 09UFD2:
01-0CT-1996 (PPL 34, Created)
20-MUG-2001 (PPL 40, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
PHOSPHATIPYLINYSITOL, 3-KIHASE VPS34 (EC 2.7.1.137) (P13-FIHASE)
(PTDINS-3-KINASE) (P13K) (VACUOLAR SORTING PROTEIN 34).
VPS34 OPR SPAC458-05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 67; DB 1; Length 1255; 29.2%; Pred. No. 22; Live 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPP001899; Gram_pos_anchor.
Pfam; PF00146: Gram_pos_anchor: 1.
ProSITE: PS00343: GPAM_Pos_aNGHORING: 1.
Repeat: Transmembrane: Gell *all: Signal.
SIGNAL 48 1255 MURAMIDASE_PELEASED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW; DCF7E55242F14341 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (FOTENTIAL).
MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
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Schizosaccharomycetales: Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
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LAPGE.
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LARGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMALL.
Streptococcus suis type 2.";
Infect. Immun. 60:2351-2357(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LARGE
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Best Local Similarity 29.27
Matches 28: Conservative
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IRANSMEM
DOMAIN
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                                                                                                                                                                                          MEDLINE=95290763; PubMed=7772832; Kimura R., Usui T., Yoshida M., Kimura K., Miyake S., Makuuchi M., Morita R., Usui T., Yoshida M., Harinouchi S., Fukui Y.; Pikui Y.; Phosphatidylinositol-3 kinase in fission yeast: a possible role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP 1-PHOSPHATIDYL-1D-MYO-INOSITOL, 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helickatier pyloti 199 (Campylohacter pylori 199).
Bacteria: Proteobarteria: epsilon subdivision: Helicobacter group;
Helickatier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHVY BAVKEFKPPYLSKGTDYCSVVIIVDQTNVKLICLLFSGNYEALPIIYKNGDIVRFH
                                                                                                                                                                                                                                                                                                                                                                                               stress responses.";
Biosci. Biotechnol. Biochem. 59:678-682(1995).
-!- FUNCTION: PHOSEPHAILDYLINOSITOL 3-KINASE HOMOLOG REQUIRED FOR
VACUOLAR SORTING AND SEGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 801;
Harris D., Lyne M., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1. SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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L -> 1 (1N REF. 3).
S -> T (1N REF. 3).
520571E1475CC341 CRC64;
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30-MAY-27-0 (Rel. 39, Last sequence update)
20-AV3-27-1 (Rel. 39, Last sequence update)
20-AV3-2-01 (Rel. 40, Last annotation update)
FUNE F REDIGES
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9; Mismatches
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Harity 29.9%; Pred. No. 15
Conservative 9; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI3K/PI4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AL358272; CA893847.1; -. InterPro: IPP0002430; P13Ka_C2, InterPro: IPP001263; P13Ka, InterPro: IPP000403; P13_P14_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  801 AA: 92135 MW;
                                                                                                                                               SEQUENCE OF 138-801 FROM.N.A.
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Best Local Similarity
Matches 23: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SIRAIN=26695 / AICC 700392;
SIRAIN=26695 / AICC 700392;
SIRAIN=27304467; PubMed=202185;
MEDLINE=77304467; PubMed=202185;
Tomb J.-F., White D., Kerlavage A.P., Clayton P.A., Sutton G.G., Fleischmann R.D., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Oudackenbush J., Zhou L., Kirhness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Gloriek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney D., Utterback T.R., Peterson J.F., Kelley J.M., Cotton M.D., Weidmen J.M., Fujii C., Bowman C., Watthey L., Wallin F., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Frasor C.M.,
                                                                                                                                 Gaps
 SEQUENCE FPOM N.A.
MEDLINE-99120557: PubMed-9923682;
MEDLINE-99120557: PubMed-9923682;
MAID R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doid P.C., Smith D.R., Noonen B., Grild B.C., deJonge B.L., Carnel G., Tumnino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang O., Taylor D.E., Vovis G.F. Irust I.J.;
                                                                                                                                                                                                                                                                                                                                           EMBL: AE001471; AAD05938.1; -.
InterPro: IPR003593: AAA.
InterPro: IPR001939: AAA_subfam.
InterPro: IPR001939: AAA. 1.
SMART: SM00382: AAA: 1.
DNA repair: SOS response: AIP-binding; DNA recombination; Helicase:
                                                                                             "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.":
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision: Helicobacter
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 66; DB 1; Length 336; 35.4%; Pred. No. 6.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 FFKPPYLSKGIDYCSVVTIVDQINVKLTCLLFSGNYEALPIIYKM3DI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIP (POTENTIAL).
4096B1AA18CA4416 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 35, Created)
15-JUL-1998 (Pel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RUVB OR HP1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 336 AA: 37280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.4%
....hos 17; Conservative
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ID RUVB_HELPY
AC 025599;
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between the Saiss Institute of Bioinformatics and the EMBL outstation the European Pioinformatics Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/creenlan email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   this SWISS-PR-I entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wai modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to licensedisb-sib.ch).
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--- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
THE COMPLETE GROOME SEQUENCE Of the gastric pathogen Helicobacter Pine complete genome sequence of the gastric pathogen Helicobacter Hature 388:530-547(1997).

1. PUNCTION: HIE BUYN-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES CRUCIFORM: HIE WAY-RUVB COMPLEX IN SUPERCOLLED DNA WITH PALLINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOLLIDAY JUNCTION HIGHATION BY LOCALIZED DENATURATION AND REAMMELING (BY SIMILARIY).

1. SUBUNIT: FORMS A COMPLEX WITH RUVA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: Ff00004: AAA: 1.
SMAKT: SM00382: AAA: 1.
DNA repair: SCS response: AIP-binding; DNA recombination: Helicase:
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PEDELINE-2215-79: FubMed-1617731:
Galinski M.P., Hedina G.G., Ingravallo P., Barnwell J.W.;
"A reticulogice-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%: Score 55; DB 1; Length 335; 35.4%; Pred. No. 6.4; tive 8; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 FFGPPGLGK-TSISHIIAKEMETNIKII------AAPMIEKSGDL 95
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: 4FA54074AF5F35A0 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01.APR-1993 (Rel. 25, Created)
01.APR-1993 (Rel. 25, Last sequence update)
01.OCT-1995 (Pel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax (strain Belem).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPP(0.2593: AAA.
InterPro: IPP(0.1939: AAA_subfam.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onery Match
Best Local Similarity 35.4'
Matches 17: Conservative
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between the Saiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no "any modified and this statement is not removed. Usage by non-profit institutions are long as its content is in no "any modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.nh/announce/or send an email to license@lsb.ch).
                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tra-heophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots: Fosidae:
eurosids II; Brassicales: Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                      492 NLIVIEKNELNGIDSTIINIEGALKESK------GN 521
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STRANS-CV. COLUMBIA:
MEDIATNS-CV. COLUMBIA:
LIN X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town G.D.,
Lin X., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum I.V.,
Fujil G.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum I.V.,
Hoffat K.S., Cronin L.A., Shen M., VanAken S.E., Ummayam L.,
Hoffat K.S., Groin L.A., Shen M., VanAken S.E., Ummayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy I.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D..
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M..
                                                                                                                                                                                                                                                                                                 34; Gaps
                                                                                                                                                                                                                                                                                                                                                          8 NYIYIPLNQLKG--GIIVNVYGVVKFFKPPYLSKGTDYCSVVIIVDQINVKLICLLFSGN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE GLUTATHIORE S-TRANSFERASE ZETA-CLASS 2 (EC 2.5.1.18).
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                                                                                                  1251 1251
1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
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106BDC8EF3E745BF CRC51:
                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 YEALPIIYKNGDIVPFHRLKIQVYKKETOGIISSGFASL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 11.6%: Score 66: DB 1
Best Local Similarity 26.3%; Pred. No. 29:
Matches 26: Conservative 11: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 AA
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InterPro: IPP000521: GST.
Pfam; PF00043: GST: 1.
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24897 MW;
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                            Malaria: Peceptor: Membrane.
NON_TER 1 1251
NON_TER 1251 1251
SEQUENCE 1251 AA; 143741
EMBL; M88058; AAA29744.1; -.
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Gaps

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33; Indels

18; Mismatches

11.5 Fest Local Similarity 21.17 Matches 28: Conservative

11.5%; Score 65; DB 1: Length 221: 21.1%; Pred. No. 5.1;

Search completed: April 12, 2002, 08:33:38 Job time: 22 sec

us-09-816-248-5.rpr

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April 12, 2002, 08:33:15; Search time 14.3 Seconds (without alignments) 580.631 Million cell updates/sec
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1 MSLVPAINYIYTPLNQLKGG......KKETQGIISSGFASLIFEGT 109
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            219241 seqs, 75174552 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result leing printed, and is derived by analysis of the total score distribution.

SUMMARIES

telomere binding procedures binding procedures binding proporbetical prote procedures prote procedures protected by the bigging protected protecte reticulocyte-bindi OPF MSV077 hypothe pricable quitathio membrane transport DMA primase [impor hypothetical prote anxin reponsive-li Description 138425 \$22581 \$3524 A41221 A41221 A81220 A83897 S76954 C659849 C659849 C659849 C65338 B83723 129589 129589 129589 172497 172497 175253 175253 178585 178585 ΠD Query Match Length DB 65 65 65 65 65 65 65 72.5 44.5 69.5 69.5 68.5 67.5 67.5 65.5 65.5 65.5 66.5 114 112 104.5 97 90 85 Score Result No.

A:Genetic r. Po: SGC5

T28238 B84436

carbamoy1-phosphat	conserved hypothet	immunophilin FKBP4	argininetRNA lig	competence locus E	ORF11 protein - Au	Acorf-12 protein -	hypothetical prote	methyltransferase	probable receptor-	hypothetical prote	preprotein translo	coatomer complex a	carbamoy1-phosphat	protein kinase C,	hypothetical prote
T11616	F69298	A55320	A64131	F70173	B36778	D72851	G71730	T51708	A84518	H72257	E71669	ERHUAH	553602	H64573	E71539
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30	<u>ر</u> ر	32	33	e) E)	ιń M	3.5	37	38	55	40	41	42	₹ 7	*! *!	4) n)

ALIGNMENTS

PESULT 1	hypothetical protein SPAC26H5.06 - fission yeast (Schizosaccharomyces pombe) C;Species: 8-hizosaccharomyces pombe C:Species: 8-hizosaccharomyces pombe C:Date: 02-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000	C.Accession: 18442 R.Oliver, K.: Harris, D.: Barrell, B.G.: Rajandream, M.A.: Wood, V. submitted to the EMBL Data Library, September 1997 A.Reference unaber: 221748	A:ACCESSION :18442 A:Status: p:eliminary: translated from GB/EMBL/DDBJ A:Molecule ';pe: DNA	A; Residucs: 1-535 <011> A; Residucs: 1-535 <011> A; Cross-reforences: EMBL: 299126; PIDN:CAR16192.1; GSPDB:GN00066: SPDB:SPAC26H5.06 A; Experiment: 1 source: strain 972h:: crismid c26H5	C:Genetics: A:Gene : SPD::SPAC26H5.06 A:Man nosit: 1: 1: 1	A;Introns: 11/1 C;Superfamily: Schizosaccharomyces hypothetical protein SPAC26H5.06	Ouery Match Best Local Similarity 34.4%; Pred. No. 0.00022; Matches 31; Conservative 18; Mismatches 35; Indels 6; Gaps 3:	Oy 18 KHITINNVGVVKFFKPPYLS-KGT-DYCSVVTIVDQTNVKLTCLLFSGNYEALPI 71	Oy 72 IVENCEDERERIQUERED OF 101 1	RESULT 2 S22581 telomerc-H: Why protein alpha chain - Stylonychia mytilus C:Species: 22-Ylonychia mytilus C:Date: 22-H:1993 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999 C:Accession: S22581	Refeng, G.: "Ach, 18, 1991 Rucleic Rucleic Review of the Marchine Reference cumber: \$22580; MUD:92051290 A:Reference cumber: \$22580; MUD:92051290	A.Accesion: \$22581 A.Status: p: liminary A.Moleculor 'Tre: DNA A.Residune: '-493 <fan></fan>	A. Cross-refreences - EMPL: X41749: NID: 010194: PID: 0578501	
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Cispecies: Euplotes crassus
Cispecies: Euplotes crassus
Cispecies: Euplotes crassus
Cispecies: 13-3an-1995 #sequence_revision 13-Jan-1995 #text_change 07-Dec-1994
Cispecies: 335525
R:Wang, W.: Skopp, R.: Scofield, M.: Price, C.
Mucleic Acids Res, 20, 5621-5629, 1992
A:Title: Euplotes crassus has genes encoding telomere-binding proteins and 'alomere-!
A:Reference number: S35524; MUID:93126105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Ille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A84422; MUID:20083487
A:Accession: A84445
A:Accession: A84445
A:Status: preliminary
A:Molecule type: DNA
A:Pesidues: 1-318 <STO.
A:Cross-references: GB:AE002093; NID:94755192; PIDN:AAD29059.1; GSPDB:GN00124
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                                                                                                                                                                                                                                                                                                                                                     26 YGVVKFFKPPYLSKGTDYCSVVIIVDQT------NVKLTCLLFSGNYEALPIIY 73
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                                                                                                                                                                                                                           12;
                                                                                                                                            Length 495;
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                                                                                                                                                                                                                  30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
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A:Cross-references: EMBL:M96819; NID:q159025: PID:g159026
                                                                                                                                   17.1%; Score 97; DB 2; 30.9%; Pred. No. 0.014; iive 14; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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115 RAGDIIRVHRATERIYNGQRQ 135
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    C:Keywords: DNA binding: nucleus
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C:Reywords: DNA binding: nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 KNSDIVRFHRLKIQVYKKETQ
                                                                                                                                                                                                                      Conservative
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A:Gene: At2q05210
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Cispedies: Emplotes crassus
Cispedies: Emplotes crassus
Cispedies: S3524
RWang, W.; Skopp, R.; Scofield, M.; Price, C.
Nucleic Acids Pes. 20, 5621-5629, 1992
A.Title: Emplotes crassus has genes encoding telomere-binding pro: ins and telomere-bin: A.Reference number: S3524; MyID:93126105
A.Reference number: S3524; MyID:93126105
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-446 <WAND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                         2:
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                        -- 53
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                                                                                                                                                                      Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 NYIYIPLNQLK---GGIIVNVYGVVKFFKPPYLSKGID-YCSVVTIVDQINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                               6 AINYIYTPLNO--LKGGTIVNVYGVVKFFKPPYLSKGIDYCSVVTIVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: EMBL:M96818; NID:q159023; PID:g159024 C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary
A:Molecule type: mPNA
A:Residues: 1-310,'S',312-455,'E',457-495 <GP2>
A:Cross-references: GB:M68939; NID:9159813; PID:9159814
C:Genetics:
                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104.5; DB 2;
Pred. No. 0.0019;
14; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 QTNVKLICLLESGNYEALPIIYKNGDIVRFHRLKIQVYKKETQ
                                                                                                                                                         Ouery Match 19.8%; Score 112; DB 2; Best Local Similarity 29.1%; Pred. No. 0.00033; Matches 30; Conservative 18; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 LTCLLFSGNYEALPIIYKNGDIVRFHRLKIOVYKKETQ 94
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Best Local Similarity 33.7%;
Matches 33; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genetic code: SGC9
A;Introns: 9/3
C;Keywords: DNA binding: nucleus
A;Introns: 32/3
C;Keywords: DNA binding: nucleus
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coperies: Bacillus suttilis
Cispecies: College of State o
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A.Residues: 1383 - KKAN>
A.Cross-references: EMB: D90917; GB:AB001339; NID:g1653836: PIDN:BAA18876.1: PID:g165
A:Cross-references: EMB: D90917; GB:AB001339; NID:g1653836: PIDN:BAA18876.1: PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: conserved hypothetical protein ycic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 5803
A:Variety: PCC 5803
C:Date: 25-Apr-1997 *sequence_revision 25-Apr-1997 *text_change 20-Jun-2000
C:Accession: S75964
R:Kaneko, T:: Sato, S:: Kotani, H.: Tanaka, A.: Asamizu, E.: Nakamura, Y:: Miyajima.
C: K:: Okumura, S:: Shimpo, S:: Takeuchi, C.: Wada, T.: Watanabe, A.: Yamada, M.: Vas.
DNA Res: 3, 109-135, 1995
A:Ititle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                 17: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 NYILSWQOGLKTAVLVNEFGEI------GIDN-ELVIASDKNMVELSNGCVCCTIN 87
                                                                                         -PYLSKGTDYCSVVTI 40
                                                                                                                                                                                                                                                                                           875 ADHTARNKITLGGNLCANIIYRETALPLLINSOVVIASRIGLKTOPFIEMFOG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 383;
                                                                                                                                                                                                                                  50 VDQT-NVKLT-----CLLFSGNYEALPITYKNGDIVRFHR--LKIQVYKKETQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 EDLVEAVYK----VLEREOKIDYLVVETIGLADPLPVALTFLGT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5; DE
Pred. No. 9.1;
                                                                                                14 INQLKGGTIVNVYGVVKFFKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
pred. No. 19;
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A.Reference number: S74322; MUID:97051201
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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   25.48;
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Rest Local Similarity 25.4%
Matches 29; Conservative
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Best Local Similarity
Matches 29: Consery
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A.Status: prelimbry
A.Molecule type: DNA
A.Residues: 1-1054 <STO>
A.Cross-references: GB.AP001513; GB:BA000004; NID:g10174345; PIDN:PAB05696.1; GSPDB:GN:7
A.Cross-references: GB.AP001513; GB:BA000004; NID:g10174345; PIDN:PAB05696.1; GSPDB:GN:7
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Princedors, Locar, J.R.: Palm, C.J.; Federspiel, N.A.: Kaul, S.: White. O.: Alonso. Chin, C.W.: Chung, M.K.: Conn, L.: Conway, A.B.: Conway, A.R.: Crossy, T.H.: Dewar, K.: ansen, N.F.: Hudbes, B.: Huizar, L.
Anutre 408, e16,-e16,-2000
A. Huizar, J.: Johnson-Hopson, C.: Khan, S.: Khaykin, E.: Kir, C.
A.: Li, J.H.: Li, Y.: Lin, X.: Liu, S.X.; Liu, Z.A.: Luros, J.S.: Maith, F.: Marziali, P.: Rathors: Salzberg, L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, A.M. Hu, D.: Yu, G.: Fraser, C.M.: Vener, J.C.: Davis, R.W.
A. Arithers: Salzberg, S.L.: Schwartz, J.C.: Davis, R.W.
A. Arithers: preliminary
A. Accession: B86210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein BH1977 [imported] - Bacillus halodurans (strain G-125) hypothetical protein BH100 halodurans (Species: Bacillus halodurans C.Species: Bacillus halodurans C.Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 31-Dec-2000 C.Accession: A83897 hypothetic Acids Res. 28, 4317-4331, 2000 A.Hitle: Complete genome sequence of the alkaliphilic bacterium Barillus halodurans A.Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ċ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein F22G5.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LLPLSGFISLDGGLQADESPYTEPLTKLFFTSDADFIKSGKSGKIQNVPG-MEYIKPYTV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YT-PLNQL------34
                                                                                                               VNVYGVVKFFKPPYLSKGIDYCSVVTIVDQT -- NVKLTCLLFSGNYEALPIIYKMGDIVR 89
                                                                                                                                                      24 VSLJGJVLEORREPKOCRNNDWICTLRIJDDIYPSPGLIVNVFSKTLEOLPQIKNHDGAIL 93
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 -PYLSKGIDYCSVVIIVDQIMVKLICLLFSGNYEAL-------PIIVKNGDITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 LRYFPDGVPNCYTLIVIOGINYLIVAMFTYGHYDNLHTHPKFDLYLGPNIMTIVDI. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41:
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                                                     Indels
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                     No. 0.15;
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                                                         Mismatches
                     Pred.
                                                     16;
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ilarity 24.6%;
Conservative 15
                     30.48;
                                                         Conservative
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Best Local Similarity
Matches 29; Conserv
                         Best Local Similarity
                                                                                                                                                                                                                                                                  81 FHRLKIOVY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: G
C;Genetics:
A;Gene: F22G5.6
A:Map position: 1
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DB 2;

Score 71.5:

12.5%;

Ouery Match

17;

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A:Accession: B83723
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1.306 <STG>
A:Experimental source: SB:AFF001509: GB:BA000004; NID:g10173176; PIDN:BAB04305.1: GSFDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GB:AE002030; GB:AE000513; NID:96459692; PIDN:AAF11467.1: PID:9645
A.Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA gyrase, subunit A - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Species: Deinococcus radiodurans
C:Species: Deinococcus radiodurans
C:Species: D. Eisen. 1999 *sequence_revision 03-Dec-1999 *text_change 17-Mar-2000
C:Accession: E75398
R:White, O.: Eisen. J.A.: Heidelberg, J.F.: Hickey, E.K.: Peterson, J.D.: Dodson, R.J.
M: Shen. M: Vanathevan, J.J.: Lam, P.: McDonald, L.: Utterback, T.: Zalewski, C.: Science 286, 157-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250: MuID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BH0546 [imported] - Bacillus halodurans (strain C-125) cispecies: Bacillus halodurans cispecies: Bacillus halodurans cispecies: Bacillus halodurans C:Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 31-Dec-2000 C:Accession: R83723 R:Takani, W.: Makasone, K.: Takaki, Y.: Maeno, G.: Sasaki, R.: Masui, N.: Fuji, F.: Pritle: Complete genome sequence of the alkaliphilic hacterium Bacillus halodurans A:Reference number: A83550: MUID:20263314
                                                                                                                                                                                                                                                972 PLDNYEKLLKNRYIPIEDLEEWDKESEAVLJGVITELKVKK----TKNGDYMAVFNLVDK 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699 MALVPG-----NDEEGELLAISECGLGKRTKVSDYPSKGRGGLGVITLDVTDKTGKL 750
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                                                                                                                                                                                                      5 PATHY -----IYTFLNQLK -----GGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Map position: 1
C:Superfamily: DNA topoisomerase (AIP-hydrolyzing) chain A: phage T4
                                                                                                                     Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 812;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
      C:Genetics:
A:Gene: dnaE
C:Superfamily: DNA-directed DNA polymerase III alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                        ; Pred. No. 34;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches
                                                                                                                   69.5; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58.5; Pred. No. 29;
                                                                                                                     Score
Pred.
                                                                                                                   12.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; 27.0%;
                                                                                                                   Query Match 12.3%
Best Local Similarity 29.3%
Matches 22: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0uery Match 12.19
Best focal Similarity 27.09
Matches 2755 Conservative
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                                                                                                                                                                                                                                                                                            53 INVKLICLLESGNYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary
A:Molecule type: DMA
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A:Sene: BH0584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Peference number: A70300: MUID:98196666
A:Accession: B70387
A:Status: preliminary: nucleic acid sequence not shown: translation not shown
A:Moleculo type: DNA
A:Pesidues: 1-1151 AQE>
A:Experimental source: strain VF5
A:Experimental source: strain VF5
A:Cross-references: GB:299110; GB:AL009126; NID:92633472; PIDN:CABI3057.1; PID:e1183230;
A:Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                              5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Aquifex aeolicus
C:Date: 08-May-1998 *sequence_revision 08-May-1998 *text_change 18-Jun-1999
C:Accession: B70387
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                                                                                                                                                                                                                                                                     22 IVNVYGVVKFFKPPYLSKGIDYCSVVIIVDOINVKLICLLFSG---NYEALPIIYKN--- 75
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                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G.; Warren, P.V.; Gaasterland, T.; Young,
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                                                                                                                                                                                  12.3%; Score 69.5; 1
28.0%; Pred. No. 12;
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75 DSALKRFAEKEVPOFOKETKDV 96
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                                                                       A:Gene: yjeA
C;Superfamily: nodB homology
F;283-428/Domain: nodB homology
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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A; Residues: 1-885 <STO>
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hyperbetical protein F25H5.7 - Caenorhabditis elegans
C.Species: T1345
C.Species: T1345
F.Steward, C.
Submitted to the EMBL Data Library, October 1995
A.Speciesion: T21365
A.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 NYMHL-LDHLKANTIDATVWNIDEIGVIPFNVOPLISETALSYETEMTEAVVVIREDNKK 277
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                                                                                                                                                                                                                                                                                                                                                                                 8 NYIYIPLNOLKGGII-----VNVYGVVKFFKPPY----LSKGIDYCSVVIIVDOINVK 55
                                                                                                                                                                                                                21; Gaps
Overy Match
Best Local Similarity 29.2%; Pred. No. 11;
Matches 25; Conservative 14; Mismatches 28; Indels 27
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   April 12, 2002, 08:33:16 ; Search time 23:55 Seconds (without alignments) 341.251 Million cell updates/sec
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Copyright (c) 1993
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human iolyFeptide	Human protein sequ	Human protein sequ	Human protein sequ	Arabidopsis thalia	Нутап тапѕтетргап	Human colon cancer	Cowdria ruminantiu	Cowdria ruminatium	Major antigenic pr	A. aeolicus AASEQ5
	OI	AAM40125	AAB92742	AAB93478	AAB95120	AAG58505	AAY13942	AAG75511	AAW51088	AAB36182		
	EQ.	. 22	22	22	22			22			1 , 22	
	Length	534	534	634	634	457	383	410	287	287	287	1161
giệ.	Query Match Length DB ID	100.0	100.0	100.0	100.0	15.4	13.1	13.1	12.4	12.4	12.4	12.3
	Score	567	567	557	567	87.5	74	7.4	70.5	70.5	70.5	5.69
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A. aeolicus AASEO5 Muramidase release H. pylori GHPO 578 Merozite apical-en Merozoite apical-e Cosmid CHRIM5 enco Arabidopsis thalia	Arabidopsis thalia S. frugiperda immu Human ST receptor Human ST receptor S. epidermidis ope S. epidermidis ope H. pylori GHPO 163 Chlamydia trachoma Bovine ribonucleas H. pylori secreted EpiB protein. Sta S. epidermis readi H. influerase stra Haemophius influerase stra GryllA insecticidida CryllA insecticidida	w		cytostatic; gene therapy; cancer; ; central nervous system; CNS; trington; s disease; haemostatic; ager Syndrome; chemotactic; ening; arthritis; inflammation;		
	AAMG8010 AAW68010 AAW32010 AAW3731 AAG82986 AAG82986 AAG829865 AAW38855 AAW38855 AAW38855 AAW3885 AAW3833 AAW1837 AAW1830 AAW1830 AAW1830 AAW1830 AAW18266 AAY96212 AAW362166		3270.	ressant; europathy ease; Hur s; Shy-Dr drug scre		
1004404177888888888888888888888888888888	238 21 412 20 1073 18 2073 19 2073 22 355 22 355 22 356 19 403 20 122 21 1222 21 702 21 702 21 703 21 703 21	815 1328 : Protei	st entry) SEQ ID NO	immunosuppus system; ne inson's disc al sclerosia combolytic;		00WO-US34263 00US-0488725 00US-0552317 00US-0552312 00US-0652312 00US-065245 00US-065345 00US-065345
	5 111 4 4 11 11 11 11 11 11 11 11 11 11 1	.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1	25: -2001 (fir polypeptide	nootropic: ral nervou: er's: Park phic later netic: thr nia.	3312 2001	2000; 20 2000; 20 2000; 20 2000; 20 2000; 20 2000; 20 2000; 20 2000; 20
φ ν φν . φνφ . φνφ . γ + γ + γ + γ + γ + γ + γ + γ + γ + γ	22 22 22 22 22 22 22 23 23 23 23 23 23 2	60 60 60 1 12 12 13 14 14 14 14 14 14 14 14 14 14 14 14 14	22-0CT iuman	(X Human: noot (W peripheral (W Alzheimer's (W amyotrophic (W chemokinetl (W leukaemia.	KO2001 26-JUL	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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Yamamoto

Salto K, Ya Otsuki T;

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The present invention describes primer sets for synthesising 5602 compliance in the specification. Where a primer set compliance in the specification. Where a primer set compliance in the specification. Where a primer set to the complementary strand of a polynucleotide whith comprises one of the 5602 nucleotide comprises at least 15 nucleotides: or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the polynucleotide which comprises a 1'-end sequence. Where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs is the primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs represent human cDNA sequences: AAB92446 to AAB13628 and AAB95893 represent human amino acid sequences: and AAB92802 co AAB92802 represent human amino acid sequences: and AAB92802 co AAB92802 represent buman cDNA sequences: and AAB92802 co AAB92802 control of the control of sequences.
                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer: detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 567; DB 22; starity 100.0%; Pred. No. 5.6e-63; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                9; SEQ ID 11188; 2537pp + CD ROM; English
                                              Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein sequence SEO ID NO:12761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention
  (HELI-) HELIX RES INST.
                                                                                                                  WPI: 2001-318749/34.
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Matches 109: Conserv
                                                                         Sugiyama
                                                                                                                                                                                                                                  full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 AA;
                                              Isogai T,
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                                                                    Ishii S,
                                                                                                                                                                                                                                                                                  Claim
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0
                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to traat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and CNNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed
                                              Wang D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                              Ren F, W
Zhang J;
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Yan: Y,
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                                              Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 3270; 10078pp; English.
                                                                 Xu C, Xue AJ
Drmanac PT;
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                                         Chen R,
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                                         Asundi V, Che
Wehrman I, Xu
Goodrich R,
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Conservative 0;
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27-AUG-1999; 93JP-0300253.
11-JAN-2000; 2000JP-0118775.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                     WPI; 2001-442253/47.
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hes 109; Consery
                                         Liu C, R
Wang Z, Y
Zhou P,
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(HYSE-) HYSEQ INC.
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09-JUN-2000:
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                                           Tang YT,
Wang J,
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Human; Нишап

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Gaps

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Length 634;

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EP1074517-A2
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                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the fagz full-length cDNAs defined in the specification, and for the determinand/or diagnosis of the abnormality of the proteins encoded b_T the
                                                                                                                                                                                                                           Yamaroto J;
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Otsuki T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 12751; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                  Nagai K,
                                                                                                                                                                                                                        Hayashi K,
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99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                       11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
  29-JUL-1999;
27-AUG-1999;
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                                        MSLVPAINYIYIPLNQLKGGTIVNVYGVVKFFKPPYLSKGIDYCSVVIIVDQTN::KLTCL 50
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c
 Length 534;
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                                                                                  61 LFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLIFEGI
Score 567: DB 22:
Pred. No. 5.6e-63;
                     Mismatches
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100.0%;
100.0%;
                     Conservative
          Similarity
                    109;
 Query Match
Best Local 9
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Human; primer; detection; diagnosis; antisense therap;; genf therapy.
                                                                                   Human protein sequence SEQ ID NO:17113.
                     AAB95120 standard; Protein; 534
                                                               (first entry)
                                                                                                                                 Homo sapiens
                                                               26-JUN-2001
                                          AAB95120;
PESULI
AAB95120
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ž 467

AAG58505 standard; Protein;

(first entry)

18-001-5000

AX EXX

AAG58505:

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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of an oligonucleotide which comprises a 1'-end sequence. Where the oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the cDNAs. The primers are also useful for the cDNAs. The primers are also useful for the cDNAs as asily without any specialised methods. AnH034508 and AAH13632 to AAH13629 to AAH13629 to AAH13632 to AAH136332 to AAH13632 to AAH136332 to AAH1363332 to AAH1363332 to AAH13643 to AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                              Hayashi K,
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T, Wakamatsu A,
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                                                                                                                                                       27-Aug-1999; 994P-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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   Protein identification: signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
   Arabidopsis thaliana protein fragment SEQ ID NO: 75533
                                                                                                                                                                                                                                 990S-0121825.
990S-0123180.
990S-012528.
990S-0125788.
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990S-0130077.
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                                                                                                  Arabidopsis thaliana
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This sequence is a human transmembrane protein of the invention.

All of the proteins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antigens for preparing antibodies against the proteins. The cDNAs can be used as probes for one diagnosts and gene sources for gene therapy, as well as for large scale expression of the proteins. The HPD1498 (see AAV1393) protein may be associated with signal transduction associated with protein can be used to treat diseases associated with phopshatidylethanolamine N-methyltransferase. The Proteins are phopshatidylethanolamine N-methyltransferase. The proteins are identified by the presence of a hydrophobic transmembrane region, knowledge of the protein function is not required, as in e.g. methods of expression cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 YLSKGTDYCSVVIIVDQTRVKL--TCLLFSGNYEALPIIYK--NGDIVRFHRLKIQVYKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; colon cancer antiqen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
cell differentiation: carcinostatic agent; probe: gene therapy; signal transduction: apoptosis: inhibitor; phopshatidy;lethanolamine N-methyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1: Page 87-89: 139pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 2.
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(SAGA) SAGAMI CHEM RES CENT.
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Best Local Similarity 26.27
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi M,
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                                                                                                                                 Homo sapiens
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Pred, No. 0.019;
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990S-0157117.
990S-0157753.
990S-0157865.
990S-0158029.
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31.2%;
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99US-0161351
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12-0CT-1
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18-0CT-1
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(UYFL ) UNIV FLORIDA.
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23-APR-1998
                                                                                                  Barbet AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB 15182;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                 animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                            cancer-associated nucleic acid molecules (N) and proteins (P). After the proteins are collectively known as colon cancer antiques. The colon cancer antiques are collectively known as colon cancer antiques. The colon cancer antiques have cytostatic activity and can be used in gene the character antiques. The colon cancer antiques and vaccine production. N and P may be used in the pre-ention, diagnosis and treatment of diseases associated with inappropriate P cassociated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing colored in a patient of the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps. By inserting the nucleic acids into a host cell and culturing the cell of the prevention: diagnosis and treatment of colorectal carcinomas and cancers. AAH37195 to AAH37204 and treatment of colorectal carcinomas and cancers. AAH37195 to AAH37204 and AAH377804 in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 YLSKGIDYCSVVIIVDQINVKL--TCLLFSGNYEALPIIYK--NGDIVRFHRLKIOVYKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEO ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAP1 gene: major antigenic protein 1; rickettsia: heartworm:
DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 74; DB 22; Length 410; 25.2%; Pred. No. 0.82; Astive 18; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cowdria ruminantium major antigenic protein 1 (MAP1).
                                                                                                                              Rosen CA:
                                                                                                                                                                                                                              Claim 11; Page 7845-7847; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW51088 standard; Protein; 287 AA
                                                                                                                                Birse CE,
                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                          28-SEP-2000; 2000WO-US25524.
                                                                   99US-0157137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cowdria ruminantium.
                                                                                                                                                        WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Owery Match
Best Local Similarity
Matches 17: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 AA;
                                                                                                                                                                    N-PSDB; AAH35016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 vangl 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 ETQGI 96
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                                                                  29-SEP-1999;
03-NOV-1999;
                   05-APR-2001
                                                                                                                                 Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW51088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Cowdria ruminatium; MAPI; major antigenic protein 1; antirickettsial: vaccine; gene therapy; Rickettsia; Ehrlichia; Anaplasma; map2; lhworf3; 4hworf1; 3gdorf3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                 Composition containing nucleic acid encoding rickettsial antigen 'useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide comprises the major antigen protein I gene (MAPI) of Cowdria ruminantium, the causative agent of heartwater in domestic ruminants. It is encoded by the MAPI gene (see AAV07176). A claimed composition comprises a nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51080-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Ehrlichia, Anaplasma and Cowdria species. The against Rickettsia. Ehrlichia, Anaplasma and Cowdria species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 PYLSK--GIDYCSVVIIVDQINVKLIC----LLFSGNYEALPIIYKNGDIVRFHRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 287;
                                                                                                                                                            McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 70.5; DB 19; 30.3%; Pred. No. 1.4; ative 19; Mismatches 18;
                                                                                                                                                                  Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 efkdiatlkiftskt-gisnpgfasatld 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 -----KIQVYKKETQGITSSGFASLIFE 107
                                                                                                                                                                  Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 15-15; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB35182 standard; Protein; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000WO-US10886.
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97WO-US19044.
                                                96US-0733230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowdria ruminatium MAP1.
                                                                                                                                                                     Burridge MJ,
                                                                                                                                                                                             Nyika A, Rurangirwa FR;
                                                                                                           (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                       WPI; 1998-251232/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowdria ruminatium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AA:
                                                                                                                                                                                                                                                                                         N-PSDB; AAV07176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W0200065063-A2.
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17-0CT-1997;
                                                       17-0CT-1996;
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                                                                                                                                                                                                                  acid vaccines containing quest to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdia sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The vaccine comprises the major antigenic protein 1 (MAPI) gene or the major antigenic protein 2 (MAVP2) gene of rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Covedia ruminatium genes designated map 2, thworf3, 44worf1, 18hworf1 and 3dorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polymocleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                           New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium. comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
 McGuire IC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 PYLSK--GIDYCSVVIIVDQINVKLTC----LLFSGNYEALPIIYKNGDIVRFHRL--- 94
                                                                                                                                                                                                            present sequence is given in a specification relating to nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Major antigenic protein 1; MAP1; vaccine: immunogenic; rickettsia:
infection; heartwater; diagnostic.
 Ganta RR, Burridge MJ, Mahan SM, McGuire
nd AL, Simbi BH, Whitmire WW, Alleman AP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McGuire IC, Burridge MJ,
SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DE Pred. No. 1.4; 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               efkdiatlkiftskt-gisnpgfasatld 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 -----KIQVYKKETQGITSSGFASLTFE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major antigenic protein 1 (MAP1).
                                                                                                                                                                             Claim 3; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04192 standard; Protein: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%;
30.3%;
Barbet AF, Bowie MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0953326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0733230
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Rurangirwa FP, Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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N-PSDB; AAS07575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cowdria ruminantium
                                                 WPI: 2000-579575/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       287 AA:
                                                                N-PSDB: AAC68699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-0CI-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CI-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04192;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04192
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7 :
                                                                                                                                                                                                       The sequence represents the amino acid sequence of major antigenic protein 1 (MAPI) isolated from Cowdria ruminantium. The MAP polynuclectides and polypeptides are useful as vaccines for conferring immunity. To rickettsia infection, including Cowdria ruminantium causing heartaster. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or acnomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermostable, nucleic acid elongation; sliding clamp protein: on: reverse transcription.
                 New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A thermostable \langle \cdot \rangle witho polymenase complex for template-dependent elongation of nucleic acids in amplification or reverse transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 pyvcagigtd---lvsvinatnpklsyggklgisysinsea--sifigg---hfbrvign 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel thermostable in vitro complex for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 PYLSK--GIDYCSVVTIVDQTNVKLTC-----ILFSGNYEALPIIYKNGDIVRFHRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%; Score 70.5; DB 22; 30.3%; Pred, No. 1.4; ive 19; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kilaer C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Page 129-134; 152pp; German.
                                                                                                                                                         Example 1; Column 11-13; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KIQVYKKETQGITSSGFASLIFE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 efkdiatlkiftskt-qisnpqfasatld 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY52037 standard: Protein; 1161 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98PE-1040771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2009-207143/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus.
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amplification:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-2000
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Pest Local S
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1161 AA;

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                                                                                                                                                                                                                                                                                                       thermostable sliding clamp protein, which is connected with it thermostable sliding clamp protein, which is connected with it thermostable sliding clamp protein, which is connected with it the thermostable in vitro accessor, which is useful for template-grounder the elongation of nucleic acids, e.g. for amplification or reverse transcription. This is useful for sequencing nucleic acids by the polymerase chain reaction or reverse transcription (RT-PCP). The complex can be used to mark nucleic acids. AAM$2000-T22084 and AM$90799 represent proteins and protein fragments used to illustrate the method of the invention.
 template-dependent elongation of nucleic acids which corrries a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable in vitro polymerase complex for template-desendes: elongation of nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable, template-dependent elongation; staple profession elongation protein; amplification; reverse transcription.
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                          24:
                                                                                                                                                                                                                                          12.3%; Score 69.5; DB 21; 29.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                            12: Mismatches
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    A. aeolicus AASE050 protein fragment.

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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-195576/17
                                                                                                                                                                                                                                          query Match
Pest Local Similarity
Matches 22: Conserv
                                                                                                                                                                                           1151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WC200008164-A2.
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07-SEP-1998;
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                                                                                                                                                                                              Sequence
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972 pldnyekllknrytpiedleewdkeseavltgvitelkvkk----tkngdymavfnlvdk 1027
                                                        Gaps
                                                                                                          5 PATNY ----- IYTPLNOLK -----GGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQ 52
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                                                  17;
Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proxyribonucleic acid encoding virulence characteristic of
Streptococcus suis - useful for antibody and polypeptide for
diagnosing and preventing infections in pigs and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is that of the muramidase released protein from
                                                        Indels
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DB 21;
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                                                  24;
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Proline-rich region"
.1256
                                                     12: Mismatches
Score 69.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
                             NO.
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                                Pred.
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12.3%;
29.3%;
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                                                                                                                                                                                                                                                         Similarity 29.3
22; Conservative
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                                                                                                                                                                                                                     53 TNVRLICLLFSGNYE 67
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867..95
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Query Match
Best Local Simi
Matches 22;
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A MAEP compound having a binding affinity for a Duffy blood group antiqen of primate red blood cells, is antiqenic for the complete protein, and may be used in diagnosis, treatment and vaccination against invasion by P.vivax and P.knowlesi.
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                                                                                                                             Merozite apical-end-localised protein (MAEP) insert 5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 12, 2002, 08:35:17 Joh time: 121 sec
                      AAR07503 standard: protein: 1254 AA.
                                                                                                                                                              Malaria: vaccine; Duffy blood group.
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                                                                                                                                                                                                  Plasmodium vivax.
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                                                                                          Q6-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnwell JW,
                                                                                                                                                                                                                                                                                                                                          96-APR-1989;
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                                                         AAR07503;
     AAR07503
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                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or trapting Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter infection; gastroduodenal disease: gastritis;
                                                                                      7 INYIYTPLNQLKGGTIVHVY-----GVVKFFKP----PYLSKGTDYGSVVTIVDGTHVKL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       products
                                      29.
Score 67; DB 13; Length 1256;
Pred. No. 29;
15; Mismatches 33; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Helicobacter polynucleotides - used to deselop
for the diagnosis, prevention and treatment of Helicobacter
infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomb
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1051 ktitfkgeeyelvrvdatangkovegetootyvyrk 1086
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(INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
                                                                                                                                        58 ICLLFSG-NYEALPII-YKNGDIVRFHRLKIQVYKK 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Al-Garawi A, Kleanthous H, Miller C,
                                                                                                                                                                                                                                                               AAW98449 standard; Protein; 335
11.88;
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97US-0833457.
97US-0881227.
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                                                                                                                                                                                                                                                                                                                                                                      H. pylori GHPO 578 protein.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         GHPO protein; Helicob
peptic ulcer disease.
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N-PSDB; AAX14168.
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                Similarity
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01-APR-1997;
24-JUN-1997;
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Query Match
Best Local Si
Matches 28;
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Wertheimer SP;

Galinski MR,

89US-0334270. 89US-0334041. 90WO-US01849

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                                                              34;
                                   Score 66; DB 11; Length 1254;
Pred. No. 39;
                                                            Indels
                                                            28;
                                                                                                   55 YEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASL 104
                                                                                                                                                    11; Mismatches
                                   11.68; 26.38;
                                 Ouery Match
Best Local Similarity 26.39
Matches 25; Conservative
1254 AA;
Segmence
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Saps

Indels

13:

Ouery Match 11.5%; Score 65; DB 1. Best Local Similarity 35.4%; Pred. No. 6.5; Matches 17; Conservative 8; Mismatches

FFKPPYLSKGIDYCSVVIJVDOINVKLTCLLFSGNYEALPIIYKNGDI 78

33 80

ò qq

DB 19: Length 336;

The present invention describes primer sets for synthesising 5602

(iul.-length cDNAs defined in the specification. Where a primer set

(iul.-length cDNAs defined in the specification. Where a primer set

(iv. the complementary strand of a polynucleotide which comprises one of

(iv. the complementary strand of a polynucleotide which comprises one of

(iv. the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination

(iv. the 5602 nucleotide comprising a sequence complementary to the

(iv. the 5002 nucleotide comprising a sequence complementary to the

(iv. the 5002 nucleotide comprises a 1-end sequence, where the

(iv. the 5002 nucleotide comprises a 1-end sequence, where the

(iv. the 5002 nucleotide comprises a 1-end sequence, where the

(iv. the 5002 nucleotide comprises a 1-end sequence, where the

(iv. the 5003 nucleotide comprises a 1-end sequence, where the

(iv. the 5003 nucleotide comprises a 1-end sequence, where the

(iv. the 5003 nucleotide comprises a 1-end sequence, where the

(iv. the 5003 nucleotide comprises a 1-end sequence)

(iv. the 5003 nucleotide comprises a 1-end sequence)

(iv. the 5003 nucleotide comprises a 1-end sequence)

(iv. the full-length comprises a 1-end sequence)

(iv. the full-length compresent thuman companion of the full-length

(iv. the full-length compresent human companion of the full-length

(iv. the full-length companion and no acid sequences; and AMH3632 to AMH3632

(iv. the present luman amino acid sequences; and AMH3632 to AMH3632 and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs . Claim 8; SEQ ID 11188; 2537pp + CD ROM; English. of the present invention.

634 AA; Sequence

.; 0 181 LKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLR 240 RIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPVVKLQNTSLYD 420 61 LFSGNYEALPITYKNODIVRFHRLKIOVYKKETQGITSSGFASLTFEGTLGAPIIPRTSS 120 61 Ifsgnyealplijykngdivrfhrikiqvykketggitssgfasltfegilgapiipriss 120 (21 KYPNPTTEDHKMVEALRVWASTHMSPSWTLLKIGDVQPMQYFDLTCOLLGKAEVDGASFL 180 1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60 0; Gaps 541 VEVMTETLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLGKSVDMIMDMFCPPGIKIDAY SKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSCH 634; Length Indels DB 22; ö 0; Mismatches 100.0%; Score 3324; 100.0%; Pred. No. 0; Matches 634; Conservative Best Local Similarity Query Match 481 181 361 121 421 361 qq Ω ογ g g ò qq ò ò ä ò ò a ò 90 ò 20 ò

specification.

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The invention relates to human nucleic acids (AAL57798-AAL61369) and the encoded polypeptides (AAM42213) with nootropic, the encoded polypeptides (AAM48642-AAM42213) with nootropic, the munosuppressant and cytostatic activity. The polymeclectides are useful immunosuppressant and cytostatic activity. The polymeclectides are useful for gene therapy. A composition containing a polypeptide or polynucleotide or polymecleotide or localised neuropathies and central nervous system diseases, such as continities and six-brane system suppression.

Calcinitation of the activity, chemotactic/chemokinetic activity, haemostatic or continity in the polymecleotide or assays for receptor activity, arthritis and inflammation, leukacmias and assays for receptor activity, arthritis and inflammation, leukacmias and continity of the order of the continity of the continit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
                                                                                                                                                                                                                                                                                                                                                                                              Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral scleroslis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, W
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Yang Y,
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Xu C, Xue AJ,
Drmanac RF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; SEQ ID NO 3270; 10078pp; English.
                                                                                             601 PWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen R,
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                                                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 3270.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                  AAM40125 standard; Protein; 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000us-0488725.
2000us-0552317.
2000us-0598042.
2000us-062312.
2000us-0653450.
2000us-065191.
2000us-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                           22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2001-442253/47.
N-PSDB; AAI59281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
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09-JUL-2000; 2
19-JUL-2000; 2
13-AGG-2000; 2
14-SER-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Match Length DB
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2: //SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:
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8: //SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:
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Gapop 10.0 ,
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3324
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  634
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AAM34264
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AAR88122
AAR88123
AAR855694
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AAM41911
AAG73583
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AAM40125
AAB93478
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  Human colon cancer
Peptide #8301 enco
Arabidopsis thalia
Tobacco mosaic vir
Tobacco mosaic vir
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Human polypeptide
Human protein sequ
Human protein sequ
Human polypeptide
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AAB92742 RESULT

AAB92742 standard; Protein; 634

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AAB92742;

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	21 21 21 21 21 21 21 22 22 21 21 21 21 2	
ALIGNMENTS	AAB18793 AAC484317 AAC484317 AAV84732 AAV84733 AAV84733 AAV84733 AAV84733 AAV857583 AAV858113 AAB18195 AAG38741 AAW25157 AAG38741 AAW25157 AAH028522 AAH28522 AAH28522 AAH28522 AAH28522 AAH213489 AAW100435 AAH70131 AAH370131 AAH370131 AAH370131 AAH370131 AAH31889 AAH47250 AAH47250 AAH47250 AAH481622 AAH48162	
	Amino acid sequenc Arabidopsis thalia Amino acid sequenc Human papillomavir Haemorrhadic enter Plasmodium falcipa Human bidquitin sp Arabidopsis thalia Tomato immunity 2 Amino acid sequenc Viral-encoded sema Human VESPK. Homo Viral-encoded sema Human PKSPK. Homo Amino acid sequenc Iluman protein sequenc S cerevisiae apopt Lottuce resistance Human PKO326 prote P	

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29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-018776.
09-JUN-2000; 2000JP-0241899.
                            Ota T, 1
Ushii S,
            WPI; 2001-318749/34.
                                                 (HEL1-) HELIX RES INST.
                                                                                                                                07-FEB-2001.
                                                                                                                28-JUL-2000;
                                                                                                                                               EP1074617-A2
                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                          Human protein sequence SEQ ID NO:11188.
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                             26-JUN-2001
                         lsogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
                                                                                                               2000EP-0116126
                                                                                                                                                                                                           (first entry)
                        Hayashi K, s
A, Nagai K,
                        Saito K,
K, Otsuki
                        Yamamoto
T;
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Primer sets for synthesizing polynucleotides, particularly the 5602

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KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL 180
                                                                           240
                                                                                                                         240
                                                                                                                                       IYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTAN 300
                                                                                                                                                                                360
                                                                                                                                                                                      RIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQNTSLYD 420
                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy
LKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLR
                                                                                                             QHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATILTDHQYLERTPLCAILKQKAPQQY
                                                                                                                                                                                                                                                    SKIWTTKNOKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGH
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, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi K,
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                                                                                                                                                                                                                                                                                        481 EDLELLDLSAPFLIQGTIHHYGTGYCT 507
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27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776.
02-MAY 2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899;
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Ishii S,
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of complementary strand of a polynucleotides which comprises one of complementary strand of a polynucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a si-end sequence. Complementary to the comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03654 to AAH13628 and AAH95331 represent human amino acid sequences; and AAH13629 to AAH13632 or FPARESENT oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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AAB92742 standard; Protein; 634 AA.

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of the pre
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T, Wakama
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A, Nagai K,
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9.1e-262;
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Tang Wang Zhao

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Liu C, Wang Z, Zhou P,

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Goodrich R,

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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2000US-0552317.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	0.00	523 523 BC002923 H	AK001935 Homo	580 AK022580	AB066545 Macac	AK026234 Homo	AL050120 Homo	AC00492	G12915	AX083744 Sequenc	AL445563	Continuation (2	AXU83/44 Seque	AL 36444 Humar	AC021378 HOMO		АС073122 Ното	AC03905/ HOMO	AC021745 Homo	AC068158 Homo	AC023852 HOI	AC041034 Homo	1141272 Capp	Continuation	Continuation	AC016314 HO	AL356485 Homo	AL592406	ALL 3 28 95	BSA ALISZY48 Caenormab H09185 Buchnera ao	292824	AC02428	96£8903V	AF284562	AC004947	ACOLS911	M10126 Lei	AC091880 Homo sa	AC092946 Homo sa	ACU6479	ALIGNMENTS		PRI	is, clone NT2RM2001544		usert sequence).	544.	.a; Craniata; Vertebrata; Euteleostomi	ss; Catarrhini; Hominidae; Homo.	.K., Suglyama,T., Otsuki,T., Suzuki,Y.	ri,T. Kaku,Y., Kodaira,H., Kondo,H., shi,M., Chiba,Y., Ishida,S., Murakawa,K.,	be,S., Kimura,K., Murakami,K.,
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TTTCACAGGCTGAAGATTCAAGTATATAAAAAGGAGACTCCAGGGTATCACCAGCTCTGGC 323		CtCtttagtggaaactatgaagcccttccaataatttataaaaatggagatattgttcgc 240 	actgaltattgctcagttgtaactaltgtggaccagacaaatgtaaaactaacttgcctg 180 	acaattgtcaatgtctatggtgttgtgaagttctttaagcccccatatctaagcaaagga 120 	atgtctttggttccagcaacaaattatatatatacacccctgaatcaacttaagggtggt 60	Ouery Match Best Local Similarity 100.0%; Score 1905; DB 9; Length 2631; Matches 1905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FDTTVAEDVI" 826 a 473 c 491 g 841 t	HEGDLD11FQDGATKTPVVKLQNTSLYDSKIWTTKNOKGRKVAVHFVKNNG1LPLSNE CLLL1EGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFIJQGTJHHYGCKQCSS LRSIQNLNSLVBKTSWIPSSVAEALGIVPJQYVFVWTFTLDDGTGVLEAYLMDSDKFF QIPASEVLMDDDLQKSVDMIMDWFCPFGIKIDAYPWLBCFIKSYNVTMSTDNDICYOI	YFDLTCQLLGKAEVDGASFLLKVWDCTRTPFDSWRVLTQDLVLEGDLSHTHRLQNLTT DILVYDMIVHVARSLKVUSFLRTYSLITTKLGSWRVLTQDLVLEGDLSHTHRLQNLTT VLPESNSDVDQLKKDLESANLTANQHSDVLCQSEPDDSFDSSGSVSLYEVERCQOLSA TILTDHQYLERTPLCALLKOKAPQOYATRAKLUSYKDRRLFGSVKLHCPKCHLLQEVD	/db_xref="G1:7022355" /translation="MSI "PATNYIYTPLNOLKGGTIVNVYGVVKFFKPPYLSKGTDYC SVTIVDQTNVKLTCLLFC:NYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFA SITFEGTI,GAPTIPFTSKKYFN™™HKMVFALRVMASTHMGES™TIKICNOMO	241928 /note="unnamed protein product" ./codon_start=1 /protein_id="BAA91568.1"	<pre>/clone-"NT2RM2001544" /clone_lib-"NT2RM2" /note-"cloning vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells."</pre>	/ce /dt /or	Unive	International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3' -end one pass sequencing and clone selection; Blelix Research Institute (supported by Japan Rey Technology Center of And Department of Vicology Lastitute of Modifical Conference of Vicology	Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of	2 (bases 1 to 2631) 1sogai,T. and Otsuki,T. Direct Submission Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao	NEDO human cDNA sequencing project Unpublished (2000)
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Series: IRAL Plate: 15 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10434050. Location/Qualifiers
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/product_"Unknown (protein for MGC:10280)"
/protein_id="AAH02923.1"
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko.Y., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Guptea,J., Ho.S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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Homo saplens, clone MGC:10280 IMAGE:3955573, mRNA, complete oc
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Catarrhini; Hominidae; Homo.
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Email: cgapbs-rëmail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951), Fax:81-438-52-3952)
NEDD human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, Institute of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk
Nishikawa,T., Nayai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki
NEDO human cDNA sequencing project
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Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mkNA,
clone_lib:NT2RM2 clone:NT2RM2001805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases to 2383)
2 (bases to 2383)
1sogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) to the DDRJ/EMBL/GenHank databases. Takao
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AK022580.1 G1:10434050
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QIPASEVLMDDDLQKSVDMIMDMFCPPGIKIDAYPWLECFIKSYNVTNGTDNQICYQI
FDTTVAEDVI"
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DILVYDNHVHVARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIR
VLPESNSDVDQLKKDLESANLTANQHSDV1CQSEPDDSFPSSGSYSLYEVERCCQLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"unnamed protein product"
/codon_start-|
/codon_start-|
/codon_start-|
/codon_start-|
/protein_id-"BAB14110.1"
/pro
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/cell_type: "tcrducarcinoma"
/clone="NT2RM2001805"
/clone="NT2RM2001805"
/clone=lib="NT2RM2"
/note="cloning vector: pME18SFL3-mRNA from uninduced NT2 neuronal precursor cells."
439. 2343
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1901.8;
Pred. No. 0;
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1260		120	Q
1638	ATTGCCCTAAATGTCATTTGCTGCAAGAAGTTCCACATGAGGGCGATTTGGATATAA	157	ф
20	cattgccctaaatgtcatttgctgcaaqaagttccacatgagggcgatttggatataatt	114	Ş
1140	cgcalccquqcaaaattquqqtcatatauqcccuqaugactatttcaqtctqttauactt	1081	р
1578			Уо
1080	cagtatttqqagaqqacaccactatqtqccattttqaaacaaaaagctcctcaacaatac	1021	Qy
1518		1459	Db
	gtatcattatacgaggtagauagatgtcuacagctatctgctacaatacttacagatcat 	961 1399	Оу
960	cagcattcagatgttatctgtcaatcagaacctgacgacagctttccaagctctggatca	901	Qy
1398		1339	db
900	agtaactctgatgtggatcaactgaaaaaggatttagaatctgcaaatttgacagccaat	841	Оу
1338		1279	
840	ttagagtttcalcttcalggaggtaccagttacggtcggggaatcagggtcttgccagaa	781	qq.
1278		1219	
780	HICTATAGCCTTCATACCABACTICABICYABITGABITCAGAGAGAATCAGACAATGTTAAGT	721	4d
1218		1159	70
720	tlagtelacgalaaccalgltealglggcaagaletelgaaggltggaagettletlaga	661	рь
1158		1099	
660 1098	CTTGTTCTTGAAGGTGATTTAAGTCACATCGATCGGCTACAAAATCTGACAATAGACATT	601 1039	Оу
600 1038	CTAAAGGTATGGGATGGCACCAGGACACCATTTCCATCTTGGAGAGTCTTAATACAAGAC	541 979	Db Oy
540	Latttgacciqacttgtcagctcttqqgcaaqcagaagtgaacggagcatcattctt	481	DP CA
978		919	
480 918	CTACTCATATCTCACCGTCTTGGACATTACTAAAATTGTGTGATGTTCAGCCAATGCAG	421 859	Оу
420	aagtattttaacttcactactgaggaccacaaaatggtagaagccttacgtytttyggca	361	Оу
858		799	
360	TTTCCATCTTTGACGTTTTCAGGGAACTTTGGGAGCCCCTATCATACCTCCCACTTCAAGC	30:	Oy
798		739	du
300	ttleacaggelgaagatteaagtatalaaaaaggagaeteagggtaleaecagetetgge	241	рь
738		679	
240 678	CTCTTTAGTGGAAACTATGAAGCCCTTCCAATAATTTATAAAATGGAGATATTGTTCGC	181 619	Оу
618		559	ф

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R. Sitel: Drail! (CACTGTG)

R. Sitel: Drail! (CACTGTG)

R. Site2: Drail! (CACTGTG)

Bescription: lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by pcR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb. The Sfil digested PCR product was cloned into distinct Drail! sites of pMELBS-FL3. Xho! sites just outside the Drail! sites can be used to isolate the cDNA insert. Libraries were constructed by singano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' and primer [CTACTGCTCTAAAAGCTGCG]; seduencing (5' and primer [CTACTGCTCTAAAAGCTGCG]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product hypothetical protein"
/product id BAB62219.1"
/protein_id BAB62219.1"
/db_xref + GT: 15011890"
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SLTFEGTLGAP I PRTSSKYRNTTEDHKNVFTLRVWASTHASPSWTLKLCVOVOPMO
RFDLTCGLLGKARVDGASFLLKVWDGTRTPFESMRVLIQDLULEGDLSHIRRQNLTI
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RECDLD I LLODGATKTPDVKLONTALYDSK IWTTKNOKGRKAAVHFVKNNG I LPLSNE
CLLL LEGGTLSE I CKLSNK NEVY I PYRSGHEDLELDLEAPET LOGT HHYGCKQCSS
I RSI JOALNSI VESK I PSSYNEVIG I VPLOYVFVMJFTLIDGTGVLEAY LMSDKFKF
O I PASSEVLMDDDLOK SMDM I MDMFC PPG I KI I DAY PWLECF I KSYNVTNJT DNO I CYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DILVYDNHVHVARSLKVGSFLRIYSLIITKLQSMNSENQTMLSLEFHLHGGTSYCRGIR
VLPETNSDVDQLKKDLESANLTANHHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSA
  (E-mail:khashl@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
Lab host: TOP10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="temporal lobe right"
/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
569. .2473
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                                                                 PME18S-FL3 (Acc.No. AB009864)
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                                                                                                                                                                                                                                                                                                                                                                                        1. 3192
/organism="Macaca fascicularis"
/db_xref="taxon.9541"
/clone="Qtra-10940"
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98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex-"male"
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Matches 1866; Conservative
                                          Lab host:
Vector:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo capping; fis (full insert sequence).
Mucaca fascicularis adult male temporal lobe right CDNA to mRNA,
Clone_lib:macaque brain cDNA library OtrA clone:OtrA-10940.
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
                                                                 agtgaaatttgcaaactctcgaacaagtttaatagtgtaattcctgtgagatctggccac 1440
                                                                                                                                                                                                                                                                                                                           1639 TTTCAGGATGGTGCAACTAAAACCCCAGATGTCAAGCTACAAAATACATCATTATATGAT 1698
                                                                                                                                                                                                                                                                                                       gaagacctggaacttttggacctttcagcaccatttcttatacaaggaacaatacatcac 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaagtgtggatatgatcatggatatgttttgtcctccaggaataaaaattgatgcatat 1800
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Macaca fascicularis brain cDNA clone:QtrA-10940, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
1 (bases 1 to 3192)
Osada.N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                        2179 AAAAGTGTGGATATGATCATGGATATGTTTTGTCCTCCAGGAATAAAAATTGATGCATAT
                                        1321 aataatggtattctcccgctttcaaatgaatgtctacttttgatagaaggaggtacactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1561 aaaacatcgtggattccttcttctgtggcagaagcactgggtattgtacccctccaatat
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
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Homo sapiens human small intestine cDNA to
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Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
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Submitted (29-AUG-20Q0) to the DDBJ/EMBL/GenBank databases.
Sugano, Institute of Medical Science, University of Tokyo,
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
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Shibahara,T., Tanaka,T. and Nakamura,Y.
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KOKAPPODYRIRKAKLSYERRILFOSYKLHCPKNNGILPLSNECLLLIEGCTLSEICKLSN
KFNSUIPVRSGHEDLELLDLSAFFLJOCTIHHYGCKOCSSLKSJONLNSLVUKTSWIP
VOLONTSLYDDSYLTMATTHADBOKFFOJFASEVLHDDDDLOKSVID
SSYNARALGJVPLOYVFWATFTLDDGTGVLENYLMDSSKFFOJFASEVLHDDDDLOKSVID
MIMDMFCPFGIKIDAYPWLECFIKSYNVTNGTDNOICYQJFDTTVAEDVI"

MIMDMFCPFGIKIDAYPWLECFIKSYNVTNGTDNOICYQJFDTTVAEDVI"

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/clone_lib-"HS1"
/tissue_type-"human small intestine"
/note-"cloning vector pME18SFL3"
135. 1289
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99.5%;
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                                                                                                                                           Martinsried, GERMANY
Clone from S. Wiemann; Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp586D211) is available at the RZPD in Berlin.
                                                                                            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is availat http://www.mips.biochem.mpg.de/proj/cDNA/.
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Mammalla; Eutheria; Primates; Catari
1 (bases 1 to 2012)
Wambutt,k., Heubner,D., Mewes,H.W.,
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                                                                                                                                                                                                                                               Direct Submission
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/organism-"Homo sapiens"
/dl_xref-"tuxon:9606"
/clone-"DKTZp566D211"
/clone_jlb-"586 (synonym: hutel).
DH10H: sites Not1 : Sall/Miul"
                                                                                 Location/Qualifiers
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              Vector pSport1; host
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                                                                                            /codon_start=1
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PWLECFIKSYNVTNGTDDQICYQIFDTTVAEDVI"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154959)
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          /tissue_type="uterus"
/map="530.1 cR from top of Chr7 linkage group"
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The Sequence of Homo sapiens PAC clone RP5-907C10
                                                                                 /note-"WUGSC:H_DJ0907C10.1, partly"
                                                                                                                                                                                                                                                            Score 408.4; DB 9;
Pred. No. 1.5e-87;
0; Mismatches 1;
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                                               /gene="DKFZp586D211"
                                                                       /gene-"DKFZp586D211"
                                                                                                                                                                                                            357 g
/dev_stage="adult"
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99.8%;
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Waterston, R.H.
Direct Submission
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Direct Submission
Submitted (14-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                      Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 14, 1999 this sequence version replaced 9::3213072.
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NEIGHBORING SEQUENCE INFORMATION: Actual start of this clone is at base position 1 of RP5-907C10; actual end is at 154959 of RP5-907C10.
Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
Jacks I to 154959)
Waterston, R. H.
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-JAN-1999) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, 5 (bases 1 to 154959) Waterston, R.
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The clone may be obtained either from Genome
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/db_xret="taxon:9606"
/chromosome="7"
/map="7q31-3q32"
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                                                                                 /rpt family-"AT_rich"
8174. .8194
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mf35f06.rl"
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6849. .7005
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5057. .5355
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3569. .3674
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3365, .3397
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DSK TWTTKNOKGKKVAVHFVKNNG LLFUSCUSLEL JEGGTLSE UKLSKNENSV LIVR
SGHEDLELLDLAPFLLJ OGTI HHYGGVESLLELJ JEGGTLSE UKLSKNENSV LIVI
VPLQYVFVMTFTLDDGTGVLEAYLMDSDKFFQ I FASEVLMDDDLQKSVDMJ MDMFCIP
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/protein_id+"AADO8852.1"
/db_xret-"G1:4176376"
/translation+"888SV$LYEVHRCQLSATILTDHQYLERTHCAILKQKALQQYR
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731 .750
/note-"similar to Mus musculus EST
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3436. .3544
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/qene="wucsc::|_bioyo7c10.1"
join(<2816. .2870,6849. .7005,8634. .8839,14398.
20470. .20558,22507. .22598,24455. .24560,25738.
/qene="wucsc::|_bio9c7c10.1"</pre>
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2297. . . 2595
                      /qenc="wuGSC:H_DJ0907C10.1"
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2596. .2760
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66. .259
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 AUTHORS
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STS.
                                                        Homo sapiens
Bouttard, G.G.,
                          Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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vp94d10.rl"
14398. .14533
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8634. .8840
/qene-"MUGSC:H_DJ0907Cl0.l"
/note="match to EST H23395 (NID:q892090) ym57q06.rl"
8718. .8839
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18466. ...18681
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13001, .13156
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10908. .11201
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10420. .10528
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12517. ..12741
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/hote-"similar to Mus musculus EST AA717633 (NID:g2729907)
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93.9%;

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lyer, L.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 208.6; DB 9; Length Pred. No. J.5e-39; 0; Mismatches 14; Indels
                                                                                                                                               Homo sapiens
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Idol.d.R., Braden, V.V., Cunningham, A.F.,
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minute(s)
minute(s)
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Pred. No. 8.8e-15;
0; Mismatches 9; Indels 0;
Weintraub, L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fultor Leckie, M.P. and Green, E.D.
A collection of 1814 human chromosome 7-specific STSS Genome Res. 7 (1), 59-64 (1997)
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each 200 uM
0.05 units/ul
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/db_xret-"taxon:9606"
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                                                                           Green, E.D.
Human chromosome 7 STSs (1997)
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Genome Technology Branch
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PCR Cycles:
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Annealing:
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ilarity 92.4%;
Conservative 0
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RESULT

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/note-"consensus sequence of A.t., L.a., and B.n. FAE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1097 tgaggteatataageeeagaageefattteagtetgttaaaetteattgeerfaaatgte 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1157 attigetgeagaagtteeaesfgaggeegtteggstatteggstatasttteeaggstggegaa 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1337 egetticaaaiyaaigitetaettiteqaiaaaqgaygiacaeteayiqaaaitiyeaaae 1396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 MVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNNAKAMCKRAKYWGWNRABVNSTCTTWKS 31.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 VTWMVRYKTDRDWSBKRMNYGMBWKNWSYDVTYYWWVWDDMCKRKVRRWVRTRGRMRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      919 Igteaateagaaretgaegaeagetttesagetetagateagtateattalaegagta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAAKNYAAAAVKAAKHIMRWANKWAMRGWIIADAAABTTDKKNNGAYTKYTTTNNNNTYRG
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PAT
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12.6%; Pred. No. 0.067;
ive 324; Mismatches 484;
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Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
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                 Sequence 22 from Patent W00111061.
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1. .1141
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synthetic construct
artificial sequence.
[ (bases | to |1141)
Kunst, L. and Clemens, S.
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                                                                                            AX083744.1 GT:13185472
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32 c
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AX083744
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3;

/standard_name."dnaA." //note-"identified by sequence similarity; possible; /note-"identified by sequence similarity; possible; similar to swiss-prof; pa4028 (DNAA_SFICI) Blastp2 p-6e-47 [c-494] /codon; start-1 /transl_table-4 /codon; start-1 /transl_table-3 /codon; start-1 /codon; start-1 /transl_table-3 /codon; start-1 /codon; start-1 /transl_table-3 /codon; start-1 /codon; sta		OKGANISM Mycoplasma pulmonis. OKGANISM Mycoplasma pulmonis Hacteria; Firmicutes; Hacillus/Clostridium group; Modlicutes; Mycoplasmataceae; Mycoplasma REFERENCE 1 (bases 1 to 32756) AUTHORS Chambaud, I., Heillq, R., Ferris, S., Harbe, V., Samson, P., Gallsson, F., Moszer, R., Lybydq, K., Wroblewski, H., Viari, A., Rocha, E., P.C. and Blanchard, A. TITLE Mycoplasma pulmonis Mycoplasma Mycopl	027 WI 11 17 17 17 17 17 17 17 17 17 17 17 17	1397 LCLCGGAACCAGTLLABTAGLGLABALLCCLGTGGAGAGACCLGGAACCACTH 1456
dene CDS .		gene GDS	qene ChS	qene Cus
Sissewyekk" Complement (37784422) /gene-"MYPU_0050" complement (37784422) /gene-"MYPU_0050" /gene-"MYPU_0050" /note-"no similarity found" /codon_start.1 /transl_table-4 /cryidence-not_experimental /product-"unknown; predicted coding region" /protein_id-"CAC13178.1" /db_xref-"G:14084418" /translation-"MERNOFSEFVOICEKNNLFYSLAFETSLSWNKGEKIDOKKHIFO VEMSIDSYKNLKKFYNNVIDNSMSINYMFLKPBFVLDKSNWINEVSFVEINILIPST LKKIKSFKSLKNLFTYQINKKNKEIKNSSLFKKIFNLFTININKAIYSIYSSKHOGFF VLSNVNEMTEKNMFLNITFKTKEIQFLNLKTRVIEEIESHFKRNYKDGYNKIIF" 4603675u /gene-"MYPU_0060"	/codon_start-1 /trans[_table-4 /evidence-not_experimental /product="conserved hypothetical protein" /protein_id="conserved hypothetical protein" /protein_id="conserved hypothetical protein" /protein_id="conserved hypothetical protein" /protein_id="conserved hypothetical protein" /db_xrei-"G1:1408417" /db_xrei-"G1:1408417" /translation="MKYIXSKIHKKVFRKLSHVKLFYKGFHNRTYLGFYNGIKVOIRL /translation="MKYIXSKIHKKVFRKLSHVKLFYKGFHNRTYLGFYNGIKVOIRL KINDIVNHEDEYKYLKNNEDYLFVNKFVVIKKWFDGEHFXANKESLKNLYDILEKFWS ONLDLAKNNWLFYKTKJIFXYLSIVEKYKDHNENDVILMWSKETHFANDKNEWLIGHE	similar to swiss-PROT:P05650 (YAAA_BACSD) Blastp2 P-6c-06 (C-45%) /coden_start i /rousi_Luble-4 /evidence-not_experimental /product."conserved hypothetical protein" /protein_id-"cAC13/76.1" /finotein_id-"CAC13/76.1" /translation-"MTILIKGEFLTIGOLIKHKINIDSGGOIKQFMQSHQVKINGKLIMTRATKINGGTTMIDDOLYTIKAQNNEE" 3088. 3771 /quae-"MYPU_0040" /note-"MYPU_0040" /note-"MyPU_0040" similar to swiss-pROT:P43055 (YLI1_MYCHO) blastp2 P-1e-28	/LTAINSTALION-"MKLFLEKSRFLERFTEKTLENTTKILESNNENYELRGAYFQVRODKILI. ISSANINISIANING KAMEYLLINGIKAKTEGGESDEJALMSLIKNI IKKOSDSILIEKKKANIPRIKLIP SDIAGSYLINILIDHEREFIDIKEGIANNOLALKTEGDEKOALKNVEAAADLSNAQELLILAS VALISIKANNITILIAZENKARIAMOKIKTEDISOEFALTINSKVVKELLSIJSMSSRTLILGE GTPELKIKSGALEIKTKVIELPYMAVENVPPAKFAREVLIHDKKELLSIJDKVSIVANE KATOKILIEN ESKEKKLKISSYMIDLGESEVESUMEVESHILKEFINANYLKES INVERKOM SILFITENKDRWVISSETHLANKOLIAALRGH" 2864. 3085 /Gene "MYPU_000" /Gene "MYPU_000"	TTILKSKINKLS" 17412862 /gene-"MYTU_0020" 17412862 /gene-"MYTU_0020" /standard_name "dnan" /standard_name "dnan" /st_noic-"identified by sequence similarity; putative; similar to SWISS#PROT:P34029 (DP3k_SPIC1) Blastp2 P-3e-14 C-4.km. (c-4.km.start-1 /rodon_start-1 /transl_table-4 /evidence-ind.cxpc-imental /product-"DNA POLYMENASE 111, HETA CHAIN" /protein_id-"CAC13175.1"

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continuation (\overline{z} or 4) or PFMALL18P2 from base 100001 (AL049185 Plasmodium talciparum
                                                                                          /translation-"MEVDQWLTQLPHILLERIVLIMAKKEVVKIAKLQFIAGOAKPGPS
                                                                                                                                                                                                                                                                                      Db 44889 FCAAATAAFTTCATATAAATAFTTTCACAAAAAAAATTTTAFAATGAAACACGTGC 44948
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                                                                                                                                                                Length 327650;
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                                                                                                                                                                                                                                Indels
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Kunst.s. and Clemens.S.
Regulation of embryonic transcription in plants
Patent: WO 0111061-A 22 15-FEB-2001;
/product.-"50s RIBOSOMAL PROTEIN L11"
/protein_id-"cAC13182.1"
/db_xref-"GI:14089422"
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                                                                                                                                                                                                                         97;
                                                                                                                                                          2.4%; Score 45.8; DB 1;
51.7%; Prod. No. 1.7;
Eive 0; Mismatches 97;
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PFMAL13P2_2
PFMAL13P2_1
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                                                                                                                                                                                                                                       104;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                            Best Local
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PFMAL13P2_1
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AX083744/C
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/product.*P60-LIKE (Mycoplasma hominis) LIPOPROTEIN"
/protesin_id-*CACL1180-1"
/dc_xrel-*G1:14084910-1"
/Lranslation-*MIKNK RILKTLPPTSTP1 LTSSLLISCGQV IDSTEKINGFTEL
KRTSTRESVLNI,YEYTVSOKYSNISIDFSTRNDOSLDDKNSOFYKOAFLAVKFYVSN
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NVDDLKKVASRD IMD IHDNIKVFTKGOPY,EPFAFDGTINLKONVVFISNDSTRKSAVY
TYRBST INBERNVENDAKKTERFCKT. VSVSTLTP.GKSNDAKPEERVVLSKADFTKL
ISYSAFNDRQLGDATNNITGYDLILLKAKRYKGVETLESNI SAFTRRQADIDOHIT IN
VASVNSSKNGRGFVGFGSLLDVSTKTSDLLST. ILGGIFKVALEIDATNIKNPEDDT IE
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ARAHFLRNITNHDFSNQSKEVEKIRKFIESEKDKNTYVELNDENIFKLKYPNNDINTK
QSEPEKTVDSMKSFFENILYPMFFDVFGSRRLKGDN"
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TPKKHSTNLKDTEEOSINHLMKTATKLAKEKTENKEPEDPYLLTINGEKAGOVVYTHTH
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avnnstagrpalpgdallenfingrnsdqvtstvdsvlnqgvlkfvkgebvftkmsn
avsfflyeqberkasenlanvfkvesgfsskipsftnblkkiideirasfekelddakkn
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/note="identitled by sequence similarity; possible;
similar to SWISS-PROT:P72083 (YHIT_MYCHR) Blastp2 P-7+-22
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similar to SWISS-PROT:P75550 (RLIL_MYCPN) Blastp2 P+6e-36
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/qene="MYPU_0070"
/qene="identified by sequence similarity; putative:
similar to TREMBL:Q49557 (Q49557) Blastp2 P=3e-15 C=29%
piscan pos. 18-28 PS00013 PROKAR_LIPOPROTEIN
Prokaryotic membrane lipoprotein lipid attachment site"
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/protein_id="CAC13179.1"
                                                                                       /note="no similarity found"
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/evidence=not_experimental
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/gene="MYPU_0070"
6759, .8180
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/qene-"MYPU_0090"
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/qene="MYPU_0080"
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                                                         /gene="MYPU_0060"
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                                                                                                                                                                                                                                                   MWWYSMNNRWYYRM 67
                                                                                                                                                                                                                                                                                                 attituatetaega 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDTAVWTBKRNYKYCYAYBWYYBMYMCKIIIWBWWRRABIIRSWNMWWVKCRNKYMVSWIIYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSAYBMAAMSMWAAGASNBYTYNWCWKMTYMCKTMTNNNNNKAWYYRTKTYAWCNNRYY 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTDWMMWTSDWBWHWYTVDYTMMRAWNNNNNNNWKHCKTTSWMWWMDHMNTHCTYGNNTW 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMWYRRYSARNWSSMARWTTRNNWWMSCBVRMRWAGTMWWRIWNNNNTDTRYYWWWKRWA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNNNNNNNNSCCTCTRMMTMRWTMKGD 623
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                                                                                                                                                                                                                                                                                                                                                    DDHBAHVKTYWYWRYDYWCAMCWMNAKAKVRTAMKHMWYYTDRYVSANNTGVRWMMMRWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMRYBKWABAYGCNNNWKDRMAHIIIIWCATNNNMMWWWYAYMIIIMHKKGKAAWTNNKTABR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cttctaaaggtatgggatggcaccaggacaccatttccatcttggagagtcttaatacaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 2.3%; Score 43.8; I similarity 9.5%; Fred. No. 4; 64; Conservative 270; Mismatches
                                                                     Drosophila meianogaster
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fruit fly,
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Eukaryota; Metazoa; Arthropoda; Trachcata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Hrachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

] (bases | to 34641)
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sequence submitted by Takis Benos, EMBL Outstation - The EBI,
Hinxton Hall, Hinxton, Cambridge, CBIO ISD, U.K.
E-mail: benos@ebi.ac.uk on behalf of the European Drosophila Ger
sequencing Consortium. For further information see the European
Drosophila Genome Sequencing Consortium's web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         du Prileon Bernard, Faculte de Medecine, 35043 RENNES Cedex, France.
2 (bases 1 to 34641)
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OKSASIYNET INVVDKKOTDYTGORKKEUM IDFRELHEIT FDEKTYMENT ISHI LACUGE
ERYFSTLDLKSGYHGVVLAERDEKEKTSFSVNGGKYEFKELFTGLRNAAG I FORT IDH
LLEOJ CKFCYVVVDDVI I FSODEEAH I KHREAFOKLRU LASEDVMLSYTDYKKTFDL
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/protein_id="cab:8458.1"
/db_stet="di-9488.82"
/LTAIS:18160+"MADDOLKEVIOAAVTAALAEGAAANKVLLDKVNSNSGOLAAAHI
TPPTVGAYAFIEINDIKCDEPLDAVKCLPEFAGAHESYVSWRQAALAAYKIFRPYDG
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ERFHSTPLELARCTKIDKGLSOTVEITMAFTOVGEKVLVKSNHSKIDKALTPLTNIJLLLVSIS
LEIHNRIGKAOYTALKARENASKOWRFTDVGEKVLVKSNHKHALGNKLTPLTNIJLLLVSIS
LASAHITDYSKAKYIPIVKGOILWMENFAYVKHSANLSEYARVVEETVGLLSHFTOSH
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LKQGKMSLLDYYDEVGKKLTLLTNKVNMSYEPVLAKGLCEKFREDALHLSTFDG11GL
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/note-"predicted using Genetinder: preliminary prediction"
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21829, .22643,22751, .23372))
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/db_xref="taxon:7227"
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Bm: EMMI: Sw: SWISSPROT Tr: TEEMAH: WP: WORNPEP: Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projets/Celegans/commpore This sequence was generated from part of betafallaledone conties of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/MOP/Chr6
RP1-166F13 is from the library RPC1-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For Inther Park Cancer Institute by the group of Pieter de Jong. For Inther Purcons, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA sequence from clone RP3-366F13 on chromosome 6 Contains ESTs, STSs, GSSs and a CpC island, Contains the OPRMI gene encoding opioid receptor mu 1, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been rinished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu), where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RRP3-366F13 It may be shorter because we sequence overlapping sections only once, except Lor a 100 base overlap. The true right and of clone RP3-366F13 is at 96110 in this sequence. The true right and of clone RP3-366F13 is at 96110 in this
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                                            sequence is ambiquous, there is an annotation using the 'unsure'
1412 atagtgtaatteetgtgagatetggeeaegaageetggaagttiitggaeettteageae 1471
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                                                                                                                                                                                                                                                                                                                                                                                                                                06 - NOV - 2000
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On Aug 29, 2000 this sequence version replaced qi:9908876.
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/nota-"AluJb repeat: matches 28. .299 of consensus"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96310)
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HTG; CpG island; mu 1; opioid receptor; OPRM1.
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/organism-"Homo sapiens"
/db_xref-"Laxon:9606"
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/clone_lib="RPCI-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURES
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                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                            SOCOR
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/note-"MADEL repeat: matches 1. .43 of consensus"
complement(join(11379, .12009,12783, .13135,63127, .63653))
/qene-"OPEMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(11474. .12009,12783. .13135,63127. .63602))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation * MSDAOLGPLRLTLSVSARTGFCKKOOEIMORRKEAAFALGTRK
VSVLIATSHSGARPAVSTMDSSAAPTNASNCTDALAYSGCSPAPSPGSWVNLSHLDGN
LSDPCGPNRTDLGGRDSLCPPTGSPSMITALTIMALYSTVCVVGLFGNFLVMYVIVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // Troco="match: cDNAs: Em:SB1111 Em:U00475 Em:U00442 Em:L13069 Em:L38645 Em:U35424 Em:L22455 Em:U19380 Em:L136915 Em:M66817 Em:D16829 Em:L225356 Em:L29301 Em:D16534 Em:L25119 Em:U04092 Em:E08874 Em:U02083 Em:E08876 Em:U3269 Em:L11056 Em:L11056 Em:L110573 Em:L110573 Em:L11058 Em:L11058
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Sw:P41143 Tr:o42324 Sw:P35372 Sw:P79350 Tr:o57585
Sw:P42866 Sw:Q95247 Sw:P41144 Sw:P41145 Sw:P35370"
                                                                                                                                                                                                                                                                                                                                                                               complement(1248, .1299)
/note-"Single clone region. Assembly consistent with restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4891, .5013
/note="FLAM_C repeat: matches 1. .123 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /nota-"MiTIH repeat: matches 40. .543 of consensus" 9914. .9956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2660 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3679. 3961
/note="AluJb repeat: matches 3. 280 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Alusx repeat; matches 1, ,308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7645, 7951
/note-"Alusq repeat: matches 1, .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998. 2125
//note="64 copies 2 mer ta 62% conserved"
2652. 2918
//note="128 copies 2 mer at 57% conserved"
2676. 2825
//note="15 copies 10 mer aatatatqtt 73% conserved"
2853. 2992
//note="13 copies 10 mer taatatataa 63% conserved"
//note="13 copies 10 mer taatatataa 63% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="16 copies 10 mer titotototo 70% conserved" 3399, .3558 /note="80 conise"? --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3275. 3370
//note="14 copies 4 mer atat 80% conserved"
3276. 33.5
/note="6 copies 10 mer tatatatgta 78% conserved"
3392. 3875
/note="71 copies 4 mer tect 61% conserved"
3398. 3557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3565. .3654
/note="9 copies 10 mer tetetette 76% conserved"
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/product="dd366F13.1"
/Aprotein.id="CA55F82.1"
/db_xref="G1:11128469"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-not_experimental
/product.*"dJ366F13.1 (opioid receptor mu l)"
complement(11379. .63653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2982, 3089
/note-"54 copies 2 mer at 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"L2 repeat: matches 2600.
8097, 8567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /qene-"OPRM1"
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Matches
                                                                                               Query Match
Best Local Similarity
22708 TTTCACTTACAAACATACTCATGGCTATACTACTGCAGGAAACTTAACGGCTTCAAATGC 22649
                   misc_teature
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notes "g copies 4 mer tyty 97% conserved"

18162. 18373

/notes "match: STS: Em:1.30054"

/notes "ll copies 4 mer ytyt 77% conserved"

/notes "ll copies 4 mer ytyt 77% conserved"

/notes "Almy repeat: matches 1. .307 of consensus"

/notes "Almy repeat: matches 2655. .2705 of consensus"

/notes "Almy repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Alusq repeat: matches 1. .300 of consensus" /note-"Alusq repeat: matches 1. .300 of consensus" /note-"Alusq repeat: matches 1. .300 of consensus" /note-"Alusq repeat: matches 1. .300 of consensus" /note-"Alusq repeat: matches 1. .300 of consensus"
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I FTILCTMSVDRY IAVCHIPVKALDFKTFIKRKI I NVORMILISKA IGI.FVHFMATTYKKO
GSJ DCTLTFSHIPTWYMENILIXICVFJITAFJIPVLJ ITVORYJLMIJRI.KISVSKMLAGSKI
KDRULRIJTRHVULVVVADJ VCOPIDJIJYJI IKALVTJ IFFTTFOTVSWIFCIALGYTN
SCI.NIVLJYAFI.DFNFKFCFKEFCT PTSSNI EQONSTRJ HONTKOHFSTANTVDHTNIHO
SCI.NIVLYAFI.DFNFKFCFKEFCT PTSSNI EQONSTRJ HONTKOHFSTANTVDHTNIHO

                                                                                                                                                                                                                                         /note* "MER69 repeat: matches 2295.
23763. .24232
/note* "match: GSS: Em:AQ793055"
24067. .24372
                                                                                                                                                                                                                                                                                                                                                                        /note-"match: GSS: Em:AQ4Z4676"
22427. .22547
/note-"MER69 repeat: matches 489. .614 of consensus"
22575. .22788
/note-"MER69 repeat: matches 662. .893 of consensus"
22769. .23087
/note-"MER69 repeat: matches 1991. .2295 of consensus"
22769. .23087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"match: GSS: Em:AQ533470" complement(22355, .22858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"match: GSS: Em:AQ777968" complement(17761. .18197)
                                                                                                                                                                                                                                                                                                                   /note="FRAM repeat: matches 2. .159 of consensus" 23247. .23438
                                                                                                                                                          /note="L2 repeat: matches 1142, .1818 of consensus"
25225, .25512
                                                                                                                                                                                                               24067. .24372
/note="Aludb repeat: matches l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(22272. .22843)
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                                                                                           2.2%; Score 42; DR 9; Length 96 H0; 49.5%; Fred. No. 13;
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                                                                              0; Mismatches 110;
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Search completed: April 9, 2002, 23:28:39 Job time: 10753 sec

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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          31.6
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1: /cgn2_6/ptodata/2/ina/5A_COMH.scq:*
2: /cgn2_6/ptodata/2/ina/5H_COMH.scq:*
3: /cgn2_6/ptodata/2/ina/6A_COMH.scq:*
4: /cgn2_6/ptodata/2/ina/GTU_COMH.scq:*
5: /cgn2_6/ptodata/2/ina/HCTU_COMH.scq:*
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      2 US-08-568-459A-11
2 US-08-487-826B-13
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3 US-09-381-862-4
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3 US-08-936-325-13
3 US-08-94-522-4
3 US-08-96-780-24
3 US-08-960-780-24
3 US-08-960-780-20
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3 US-09-073-898-20
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4626.709 Million cell updates/sec
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              Sequence 41, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 13, Applisequence 4, Applisequence 4, Applisequence 4, Applisequence 24, Applisequence 24, Applisequence 20, Applisequence 20, Applisequence 20, Applisequence 21, Applisequence 21, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 17, Ap
                                                                                                                                                          Patent No.
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Sequence 41, Appl
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uery Match 1.9%; Score 35.8; DB 2; Best Local Similarity 53.1%; Pred. No. 2.4; Matches 76; Conservative 0; Mismatches 67;

Length 2404;

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- 428 - 428	CLASSIFICATION: 536 ATTORNEY/ACENT INFORMATION: NAME: JORDIC, RODERT J. REGISTRATION NUMBER: 33,915 REFERENCE/DOCKET NUMBER: N1227-003 TELECOMMUNICATION INFORMATION: TELEPHONE: 402-333-1510 TELEFAX: 402-333-1510 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 2404 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: JINear FOLECULE TYPE: DNA (genomic)	US-08-868-577-19/c US-08-868-577-19/c Sequence 19, Application US/08868577 Fatern No. 5866698 GENERAL INFORMATION: A SOYHEAN PEROXIDASE GENE FAMILY AND AN TITLE OF INVENTION: A SOYHEAN PEROXIDASE GENE FAMILY AND AN TITLE OF INVENTION: ASSAY FOR DETECTING SOYHEAN PEROXIDASE NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: ROLINGES: 1 ADDRESSEE: ROLINGES: 1 STATE: DC COUNTRY: WASHINGLON ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: FIOPPY disk COMPUTER: LIMPEC COMPALIBLE OPERATING SYSTEM: DC-DOS/MS-DOS SOFTWARE: WORDER-CO-TINE-1907 CURRENT APPLICATION NUMBER: US/08/868,577 FILLING DATE: US/08/868,577	29 31.6 1.7 3659 1 08-08-413-118-72 30 31.6 1.7 3659 2 08-08-184-007-78 31 31.6 1.7 3659 2 08-08-184-007-78 32 31.6 1.7 3659 2 08-08-417-210A-67 33 31.6 1.7 3659 2 08-08-458-356-72 34 31.6 1.7 3659 3 08-08-458-356-72 35 31.6 1.7 3659 4 08-08-478-46-72 36 31.6 1.7 3659 4 08-08-478-08-26 31 31.6 1.7 3660 1 08-08-207-792-25 30 31.6 1.7 3660 1 08-08-207-792-25 30 31.6 1.7 3661 1 08-08-207-792-25 31 31.6 1.7 3661 1 08-08-408-124-7 41 31.6 1.7 3661 1 08-08-124-7 42 31.6 1.7 3661 1 08-08-207-729-7 43 31.6 1.7 3661 1 08-08-207-729-7 44 31.6 1.7 3661 1 08-08-207-207-221 44 31.6 1.7 3661 1 08-08-208-208-208-208-208-208-208-208-20
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305 ATTGAATATCAATCTGATAAAGCGTTAAACCCAGACAGTCAAATCTTTAAAGAATTGAAA 364

1248 atcattatatgattcaaaaatctggaccactaaaaatcaaaaagacqaaaagtaqcayt 1307

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1285 caaaaaggacgaaaagtagcagttcattttqtgaaaaataatggtattctcccgctttca 1344
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TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
                                     1405 aagtttaatagtgtaatteetgtgagatetggeeaegaagaeetggaaettttg 1458
                                                                          365 TTATTTAAAATAAATAGTCAAAAAACAATGTCAACAAGTGCAACAAGACGAATTG 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
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2421 N.W. 41st Street, Suite A-1
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APPLICATION NUMBER: US 60/029,848
FILING DATE: 80-02T-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
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Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
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                                                                                                                                                                                  Sequence 41, Application US/09074898 Patent No. 6242669
                                                                                                                                                                                                                                                Feitelson, Jerald S.
Schnepf, H. Ernest
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REGISTRATION NUMBER: 39,355
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                            Narva, Kenneth E.
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 50.0%
Matches 87; Conservative
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TELEPHONE: 352-372-5800
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EDNESS: single
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ZIP: 32606-6669
COMPUTER READABLE FORM:
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APPLICANT:
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245 CAAAAAGGCGAAAAGAAACAAGTTGTTCATTTAGAAAAAGATAAATTTAGTTCCAAAAA 304
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STREET: 2421 N.W. 41st Street, Suite A-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
ATTOHNEY/AGENT INFORMATION:
                                                                                                                                                                                                    Sequence 41, Application US/08960780
Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, Brian A.
APPLICANT: Schnepf, Brian A.
APPLICANT: Schmelts, James
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Dullum, Charles Joseph
Muller-Cohn, Judy
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REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
                                                         1308 tcattttgtgaaaaataatggta 1330
                                                                                                   228 AAATTTTAGACATTTAATTGAA 206
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MEDIUM TYPE: Floppy disk
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Matches 87; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                  US-08-960-780-41
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APPLICANT:
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US-09-046-086-1/c
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                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SECTION NO:
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MEDIUM TYPE: Diskert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wallis, Nicola G. TITLE OF INVENTION: NO. 6127 TITLE OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2488
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APPLICATION NUMBER: 60/043,489
FILING DATE: 10-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                            1012 acaqatcatcaqtatttqqaqaqacaccactatqtqcrattttqaaacaaaaaqctcct 107.
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 450 TAATAAACCATCATTGCAACAAAATAGTTGTTATACAA 413
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                                                             510 TGATATTCACGCTTTTTCATTTTTTAAAATTATCTAGCATTATTAACGATAAAGAATAACGACA 451
                                                                                                                           TYPE: nucleic acid
STKANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Falk, Stephen
REGISTRATION NUMBER:
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CLASSIFICATION:
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REFERENCE/DOCKET NUMBER: GM50025
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4000 Rell Atlantic Tower, 1717 Arch Stro
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SYSTEM: Windows 95
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Best Local Similarity 52.9%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                RECLISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHIZI.001CFI
TELECOMMUNICATION INFORMATION:
TELEPHONI: (619) 235-8550
TELEFAX: (619) 245-0176
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SU XIU-SHAMA
APPLICANT: MCLICHN, THOMAS E.
TITLE OF INVENTION: HINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND DIAASMODIUM FALCIDARUM ERVTHROGYTE BINDING PROTEINS
TITLE OF SEGUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: THM PC compatible GPEATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Fatentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
              1307 treattitotgaaaaataat 1826
                                                            ORIGINAL SOURCE:
ORGANISM: Pla
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
8200 AAAATTTTTAAAAAATAAT 8219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 164h Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LITTING DALLS
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Miller, Louis B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sim, Kim L
                                                                                                                                                                                                                                                                              Plasmodium talciparum
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                                                                                                                                                                                                                                                                                                                                       Linear
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                                                                                                                                                                                g Score 34.4; DB; Pred. No. 8.8; 0; Mismatches
                                                                                                                                                                                                                 DF 2;
                                                                                                                                                                                     66;
                                                                                                                                                                                                                 Length 8220;
                                                                                                                                                                                     0;
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US-08-487-8268-11 ; Sequence 11, Application US/084878268 ; Palent No. 5983827

GENERAL INFORMATION:

Kim I.

RESULT

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linear
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                                                                                                                                       COUNTRY:
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                                   APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ċ
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Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David S.
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-58P-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 44.4; DH 2;
52.9%; Pred. No. 8.8;
tive 0; Mismatches 66;
                                                                                                                                                                            ANDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH121.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                 MBER: US/08/487,826B
10-SEP-1993
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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8200 AAAATTTTTAAAAAAIAAT 8219
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (qenomic)
Chitnis, Chetan
                      Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 8220 base pairs
TYPE: nucleic acid
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Bost Local Similarity 52.9°
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                     NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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APPLICANT:
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TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
AJDRESSEE: Robbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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APPLICANT: Udyama, Hiroshi
APPLICANT: Abe, Kanako
APPLICANT: Keshi, Hiroyuki
APPLICANT: Matsuhisa, Akio
TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTILE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                         CURRENT APPLICATION: DC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
ATTORNEY/AATTON: 47E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: (619) 235-955
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09381862
Patent No. 6245906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 52.9
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                          STREET: 620 Newport
CITY: Newport Beach
STATE: California
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Best Local Similarity
                                                                                                                                          APPLICANT: Mandel, Gail
APPLICANT: Haleqoua, Simon
APPLICANT: Horden, Laurence A.
TITLE OF INVENTION: Section Chan
TITLE OF INVENTION: Section Chan
TITLE OF INVENTION: X-ray Dittre
TITLE OF INVENTION: Drug besign,
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
THE PERIODECARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1364 tagaaggaggtacactcagtgaaatttgcaaactctcgaacaagtttaatagtgtaattc 1423
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     5245
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ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: APPLICATION NUMBER: 25-MAK-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                               STREET: 1100 New
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OKGANISM: Streptococcus pyogenes
STRAIN: Clinical isolate SP-26-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaqqaacaatacatcactatgqatqtaaacaqtqttcta 1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTTAATATTTCTAAAGAAGAGAGTAAACATGGTTTTA 5283
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20005-3934
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                                   K
                                                                                                                                                                                                                                                                                                                                      Application US/08836325
                                                                     1100 New York Ave.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                          STERNE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (aenomic)
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25-MAR-1997
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                                                                                                                                            Peripheral Nervous Systom Specific
Sodium Channels, DNA Encoding Therefor, Crystallization,
X-ray Diffraction, Computer Modernia Modeling, Rational
Drug Design, Drug Screening, and Methods of Making and Using
Thereof
                                                                     RESSLEW, GOLDSTEIN & FOX F.L.L.C
ork Ave., N. W., Suite 600
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Fred. No. 9.5:
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US-08-836-325-14
; Sequence 14, Application US/08836325
; Patent No. 6110672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.00, best Local Similarity 53.4%;
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                        APPLICANT: Mandel, C
APPLICANT: Halecoma
APPLICANT: Horden, I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-371-2540 INFORMATION FOR SEC ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 6371 base parts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                      TITLE OF
                                                                                                                                                                           TITLE OF
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                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 tettqqaeattaetaaaattqtqaatqttcaqceaqtattttqaeetqaettqt 498
                                                                                                                                                                                                                                                                                                                                                                                                                                     459 cagcicttgggca 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                  STATE
                                                                  ADDRESSEE:
STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 0H/4
FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                COUNTRY:
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                                               Washington
20005 3934
                                                                                                                                                        INVENTION:
                                                                                                                                                                           INVENTION:
                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                       Borden, Laurence A.
                                                                                                                                                                                                                                                            Mandel, Gail
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                     Poripheral Nervous System Specific Sodium Channels, DNA Encoding Therefor, Crystallization, Sodium Channels, DNA Computer Molecular Modeling, Rational Newsign, Drug Screening, and Methods of Making and Usin
                                                                                                                                        Thereot
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APPLICATION NUMBER: US/08/749,522
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                      TELEPHONE:
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APPLICANT:
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                                                       CF.RATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: FIBER-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                  0917.0240002
                                                                                                        ADPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIPICATION: 514
PROOF APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: 08/334,029
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...orESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
GITY: Milwaukee
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                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917
TELECOMMULICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/08749522
; Patent No. 6096950
; GENERAL INFORMATION:
                                 COMPUTER: IBM PC compatible CFERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 6404 base pairs
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Best Local Similarity 53.4.
Rest Local Similarity 53.4.
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Quarles &
   COMPUTER READABLE FORM:
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STRANDEDNESS: both
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US-08-836-325-14
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COMPUTER: [B]
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TITLE OF INVENTION: No. 6204435cl Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1359 tttgatagaaggaggtacactcagtgaaatttgcaaactctcgaacaagtttaata 1414
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2421 N.W. 41st Street, Suite A-1
                                                                                                    670513.90244
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APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-00T-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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Schnepf, H. Ernost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stockhoff, Brian A. Schmeits, James
CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
ATME: Baker, Joan C.
REGISTRATION NUMBER: 35,433
                                                                                                    REFERENCE/DOCKET NUMBER: 67. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                         THLEFAX: (414) 271-3552
[NFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2781 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       (414) 277-5709
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MEDIUM TYPE: Floppy disk
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ATTOKNIY/ACHMI INFORMATION:

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US-09-073-898-24
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Best Local Similarity
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APPLICANT: Finstad-L
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                              COMPUTER: THM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-LOS
SOTWARE: Patentla Release #1.0, Version #1.30
CURRENT_APPLICATION DATA:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                    CLASSIFICATION:
                                                    FILING DATE:
                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                    CITY: Gainesville
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                  ADDRESSEE:
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REFERENCE/DOCKET NUMBER: MA-708
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DEDNESS: single
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2421 N.W. 41st Street, Suite A-J
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Pinstad-Lee, Stacey
NENTION: No. 6242669cl Pesticidal Toxins and
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Schmeits, James
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                                                                US/09/073,898
 US 60/029,848
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Pred. No. 9;
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; Patent No. 62043 8
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Best Local Similarity 49.4%; Pred. No. 9;
Matches 86; Conservative 0; Mismatche
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                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: No. 620443501 Pesticidal Toxins and TITLE OF INVENTION: Sequences Which Encode These Toxins
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APPLICATION NUMBER:
                                                                               MEDIUM TYPE: Floppy disk
COMPUTEK: JHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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              APPLICATION NUMBER: TILING DATE: 30-OC
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CLASSIFICATION:
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Schmeits, James
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MRNTION: No. 6242669el Pesticidal Foxins and Nucleotide
FENTION: Sequences Which Encode These Toxins
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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19.4%; Pred. No. 9;
tve 0; Mismatches
          APPLICATION NUMBER: US 60/029,848.
FILING DATE: 30-027-1996
ATTONEVAGENT INFORMATION:
NAME: SALIWANCHIA, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 352-375-8100
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Schmeits, James
Loewer, David
Dullum, Charles Joseph
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; Patent No. 6242669
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Narva, Kenneth E.
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Stamp, Lisa
Morrill, George
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20:
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INDIVIDUAL ISOLATE: 31J2
US-08-960-780-20
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                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pairs
TYPE: nucleic acid
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Matches 86; Conservative
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PRIOR APPLICATION DATA:
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ZIP: 32606-6669
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STRANDEDNESS:
TOPOLOGY: line
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US-09-073-898-20
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1.7%; Score 33.2; Di
Best Local Similarity 49.4%; Pred. No. 9;
Matches 86; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0H/960,780
FILING DATE: 30-0CT-1997
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                            NAME: Sanders, Jay M.
RECISTRATION NUMBER: 39,355
RECIESTER/COCKET NUMBER: MA-708C1
FELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1045 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Title:
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Maximum DB seq length: 2000000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALICNMENTS

	Source	FEATURES		COMMENT	JOURNAL.	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AL555074
/organism "Homo sapions" /db_xref-"taxon:9606" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"CS0DK007YG14" /clone-"blacenta" /clone-"b	3889	Email: segret@qenoscope.cns.ir, wco : www.qenoscope.cns.ir.	BP 191 91006 EVRY cedex - France	Contact: Cenoscope Cenoscope - Centre National de Sequencage	Unpublished (2001)	Full-length cDNA libraries and normalization	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	1 (bases 1 to 889)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST:	AL555074.1 G1:12896461	princ, mrna sequence. AL555074	AL555074 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK007YG14 5	AL555074 889 bp mRNA EST 16-FEB-2001	

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Tissue Procurement: AFCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arcayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: McG.clone distribution information on the Cound through the LMA.G.E. Consortium/LLNL at:
http://imago.llnl.gov
plate: LLAM11299 row: a column: ll
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Location/Qualifiers
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Tissue Procarement: AFCC/DCTPD/DTP
CDNA Library Preparation: Lite Technologies, Inc.
cDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
NJH MGC http://mqc.nci.nih.gov/
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601432077F1 NIH_MCC_72 Homo
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                                                    /clone_lib-"NII_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host-"DH10b (phage-resistant)"
/note-"Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Frimer: Oligo caverage insert size 2 kb. Library constructed by Lite Technologics."
                                                  Technologies
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/clone="IMAGE:3917299"
                                                                                                                                                                                                                                                                                            /organism="Homo sapieus"
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National Institutes of Health, M
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Unpublished (1999)
Contact: Robert St
                                                      Eukaryota; Motazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                   Vertebrata;
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           Tissue Procurement: AVCC construction Life Technologies, Inc.
CDMA Library Preparation: Life Technologies, Inc.
CDMA Library Arrayed by: Incyte Genomics, Inc.
CLOR Sequencing by: Incyte Genomics, Inc.
Clone distribution: McC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
http://inage.ill.yov.
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/lab_host="DH108"
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High quality sequence stop: 705.
Location/Oualifiers
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/organism="Nomo sapiens"
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Smail: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
National England (1999)
Contact: Robert Strausberg, Ph.D.
Emall: ggapbs-r@mail.nih.gov
Tissue Procurement: ATGC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayad by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imagc.llnl.gov
Plate: LimAM972, row: n column: Il
High quality sequence slaft:
Location/Qualifiers
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/organism-"Homo sapiens"
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Tissue Procurement: ATCC
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1 (bases 1 to 584)
NIH-MGC http://mgc.nci.nih.gov/.
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/lab_host*"Dhl0B (phace-resistant)"
/note*"Organ: Lustis; Vector: pCNV-SFORTG: Site_1: Not1.
Site_2: Sall; Cloned unidirectionally; cliqced primed.
Average insert size 2.5 kb. Library cariched for
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Note: this is a NHL_MCC Library."
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National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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MSLVFATNYIYTPLNOLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60

Query Match Best Local Matches 50

Similarity

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Score Pred. 1; Mis

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RESULT
AAB93478
The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligorod primer and an oligonucleotide complementary strand of a polynucleotide witch comprises one of the 5602 nucleotide sequences defined in the specification, where the cc cligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the ccmplementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides in gene therapy and sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides. The primers are useful for synthesising polynucleotides in gene therapy and complementary to a sequence is selected from those defined in the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are also useful for the thing and the sequences of the full-length cDNAs are sequences; and AAH13628 and AAH13633 to AAH13629 to AAH13632 represent human cDNA sequences; and AAH13629 to AAH13632 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5502 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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Ishii
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02-MAY-2000;
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2732
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Result		Query	Query		;	Description
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09Y4E4:

01-NOV-1999 (TIEMBLIEL 12, Last sequence update)

01-NOV-1995 (TIEMBLIEL 17, Last annotation update)

01-JUN-2001 (TIEMBLIEL 17, Last annotation update)

01-JUN-2001 (TIEMBLIEL 17, Last annotation update)

01-JUN-2001 (TIEMBLIEL 17, Last annotation update)

81AA0580 PROTEIN (FRAGMENT)
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EMBL: ABO11152: BAA25506 1: ...
Interpro: IPR000198: Znf_GCS.
Interpro: IPR001164: Znf_GCS.
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pfam; pF00520; phoGAP; 1.
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pfam; pF01412; ArfGaP; 1.
pfam; pF004405; REVINITACING.
pR1NITS; pR50003; pH_DOMAIN; 3.
pROSITE; pS50003; pH_DOMAIN; 3.
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Code for large proteins in vitro. :

DNA Res. 5:11-39(1998).
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RP KEDUINE=94150718.

RN Wilson R., Ainscough R., Connell M., Favello A., Fulton L.,

RA Wilson R., Ainscough R., Connell M., Favello A., Johnston L.,

RA Bonfield J., Burton Du Z., Durbin Hillier L., Latreille P.,

RA Craxton M., Green P., Hawkins T., Laister N., Latreille P.,

RA Gardner A., Kershaw J., Kirsten J., Laister N., Saunders D., Johnston R.,

RA Jones M., Kershaw C., Mcmurray A., Mortimore B., Sundtarston R.,

RA Lightning J., Percy C., Rifken L., Roopra A., R. Saunders D., Johnston R.,

RA Lightning J., Percy C., Sonnhammer E., Staden R., Waterston R.,

RA Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,

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RA Thierry-Mieg J., Thomas K., Vaudin M., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

RT elegans Ka. 72-78(1994).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
11-NOV-1999 (TrEMBLrel. 17, Last annotation update)
11-NOV-1999 (TrEMBLrel. 17, Last annotation update)
12-NOV-1999 (TrEMBLrel. 17, Last annotation update)
12-NOV-1999 (TrEMBLrel. 12, Created)
12-NOV-1999 (TrEMBLrel. 12, Last annotation update)
13-NOV-1999 (TrEMBLrel. 17, Last annotation update)
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Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda:
Eukaryota: peloderinae: Caen
Rhabditidae: peloderinae:
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peloderinae: Caenorhabditis

Chromadorea; Rhabditida; Rhabditoidea;

1217

Nature

e 358:32-38(1994) E 358:32-38(1994) CAB04180.1:

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255 LLEETN-KKWCVLEGGELSYYENDKSTTPNGTININEVICLAIHKEDEYLNTGPIE---I 310
                                                                                                                                                                                                                                105 FEGTLGAP11FRTSSKYFNFTTEDHKMVEALRVWA---STHMSPSWTLLKLCDVOPMQYF 152
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                                                                                                                                                                                                153 DLTCOLLGKAEVDGASFLLKVW---DGTRTPFPSWRVLIQDLVLEGDLSHIHRLONLTID 219
                                                                                                                                                                                356 DLIGOLFTK-DCHALDOWRKGWFAMDKSSLHF-----CLOMDEVOGDRWHLRRLOELTIS 409
                                                                                                                                                               410 THVOHSEKLDVLLLVEKGRTLYİHG-HTKLDFTVWHTAIEKAAGTDGNALODQOLSKNOV 468
                                                                                                                              258 MLSLEFHLHGGTSYGRG1RVLPESNSD-----VDQLKKDLESANLTANOH--SDVIC- 307
                                                                                                                                                                                                                                                                    , INDOINAKTICTT -- ESCHAEVTLIAKNCDIABEHETKIOAKKELOGIISSCEVERT
                                                                             529 LKSFLSDIDDALLTK---ELYPYWISALDTODDKERIKKYGA-FIRSLPGVNRATLAAII 584
                                                            353 KOKAPOOYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEG--DLDIIFQDGATKTPD 410
                            411 VKLOHTSLYDSKIWTTKNOKGRKVAVHFVKNNGILPLSNECLLLLIEGGTLSEICKLSNKF 470
                                                                                                                PIIVNSCIAFVTOYGLGCKYIYOKNGDPLHISELLESFKKDARSFKLRAGKHQLEDVTAV 528
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Best Local Similarity 99.4%;
Matches 174; Conservative
                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI51369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypurcleotides are useful in gene therapy. A composition containing a polypeptide or polypurcleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheiner's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activinyinhibin activity, chemotactic/chemokinetic activity, haerostatic assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                              genetic
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                                                                                                                                                                                                                                                        09-AUG-2001
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  (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0508408.
2000US-0532356.
2000US-023359.
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115-APR-1999
12-AFR-1999
21-AFR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA13135-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenca. The probes are useful for antenatal diagnosis of human genetic disorders.
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L-1999; L-1999; L-1999; L-1999; L-1999;	1999; 1999; 1999;	;666 ;666 ;666	999;	9999	999;	999;		999;	9999	999;	999;	999;	999;	999;	999;	999	999	, 666 , 656	, 666 , 656	: 66	9 9	999	9 9 9	999	99;	999	99,	0 0	99;	9 4	9 9 9	99;
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Best Local Similarity 20.9%;
Matches 109; Conservative 8
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                                                                                                                                                                                                                                                                                                                                 1095
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N-PSDB: AAQ62924.
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ik::tinnsnnsi----snnenve-tnlncvseragshhiyg
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AAW06556
ID AAWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: serine kinase: SRFKI: SR domain: SR family; splicing factor: cell proliferation; malignancy; psoriasis: pemphigus vulgaris: Behcet's syndrome; acute respiratory distress syndrome; leukachia: rheumatoid arthritis; AIDS; vasculitis: septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine kinase SRPK1
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87
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533
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213
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109
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89
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80..10
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520
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521
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257..2
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208..2
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172..20
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132..1
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521..5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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N-PSDB; AAT45897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated serine kinase nucleic acid encoding SRPK1 - used to develop prods. which can be used in detection and therapy, partic. for cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   247 KLOSMNSENOTMLSLEFHLHGGTS-----YGRGIRVLPESNSDVDQLKKDLESAN----
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9
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                         10
                                                                             edigtrg-yrslevl-----igsgyntpadiwstacmafelat 546
                                                                                                                                                                                                                                                                                                                                                                                           SVIPVRSGHEDLELLDLSAPFLIQGTIHHYGTGYCTP-----PICVCYDLYT
                                                                                                                                                                                               CWTSLYDSKIWTTKNOKGRKVAVHFVKNNGILPL--SNECLLLIEGGTLSEICKLSNKFN
                                                                                                                                                                                                                                         qsfseqh----
                                                                                                                                                                                                                                                                             OKAPOQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKL 413
                                                                                                                                                                                                                                                                                                                    qnlnqessfl-----slpnqdsstsqetdsctpitsev-----sdtmvcqssstvg
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61: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.8%;
                                                                                                                                                            -nkgkstagnflvn----plepknaeklkvkiadlgnacwvhkhft
                                                                                                                                                                                                                                           ---isqlqesiraeip-cedeqeqehngpld------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 
Pred. No. 0.19;
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AAY58113;

AAY58113 standard; Protein; 1112

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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                                                        Sequence
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subunit yaccine: antiviral: recombinant; vector; deno theraps
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                                                                                                                                                                          2
                             EGTLGAPIIPPTSSKYFNETTEDHKMVEALRVWASTHMSPSWTLLKLC-DVQPMQYFD---
                                                                                                                                                                       skyiyttqneipyrlqickkdikatiieiawtynlfnckklak-----kvkdaqsyi 53
                                                                                                                                                                                                                  TNYIYTPLNQLK------GGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-062458/05
DB: AAZ46368.
                                                                                                                              LTCLLFSGNYEALPIIYKNGDIVRFHRL---KIQVYKKETQGI-----TSSGFASLTF 105
                                                                                                                                                                                                                                                             l Similarity
95; Conserv
---iydksklcwikswtqqqkcsscqriysaih--
                                                                                                                                                                                                                                                                                                                                                                          1112 AA;
                                                                                                                                                                                                                                                                Conservative
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tter B. Gallili G. Michael A. Gol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enteritis virus in domesticated
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19.0%;
                                                                                   -nsdienvknlpvksitiwkkltgcvmignefktsheyieldf
                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                Score 104; DB
Pred. No. 0.58;
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birds
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urkey and in
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RESULT 1
AAB31889
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                                                                                                                                                                                                                                                                                                                                                                     Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using speci polypeptides or related nucleic acid or ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ganglioside GM2 activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human: perlecan; retinol-binding plasma protein; calgranulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid polyarthritis; lupus erythematosus; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human protein
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The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which use at least one polypeptide or polynucleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the retinol-binding plasma protein, precursor of the state of the californial protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polynucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and

uses of.

Claim 1: Page 138-152; 209pp; French.

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agius CI,
Ross BC,
         Porpherymonas gingivalis;
                                                                                                                                     AAY 34336
                                                                        25-AUG-1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-385613/32
N-PSDB; AAX91678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GAPIIPRTSSKYFNFTTEDHKMVEALRVWASTHMS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LTCLLFSGNYEALPIlYKNGDIVRFHRLK10VY-----KKETOGITSSGFASLTFEGTL 110
                                                                                                                                                                                                                  ennavegaktegsindgltkya···gdneligglidlallgsglltgealaefirrsgr 582
                                                                                                                                                                                                                                     ONTSLYDSKIWITKNOKGRKVAVHFVKNNGILPLSNECLL---LIEGGTLSEICKLSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GDLSHIHRLQHLTIDILVYDNHV--HVA----RSLKVGSFLRIYS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dspdiplnvsrsylgsdanvkki-----sshitkkvadrleeifkndrptfeekwdsl 371
                                                                                                                                                                                                                                                                              epsltelrakiaelkaeeaklldeekqkkp----eeip--
                                                                                                                                                                                                                                                                                                             APQOYRIBAKLRSYKFR--RLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKL 413
                                                                                                                                                                                                                                                                                                                                           egeailitqaefmrrmrdmaqlqpgmsfyg-elpdsynlvlntdhplidrv-lsgekesv
                                                                                                                                                                                                                                                                                                                                                                          NQHSDVICQSE----PDDSFPSSGSVSLYEVERCQQLSATILTDHQYLERTPLCAILKQK 355
                                                                                                                                                                                                                                                                                                                                                                                                        keeraevklsdteratlvkl-fear-----lprde----kkhfnvafeslga
                                                                                                                                                                                                                                                                                                                                                                                                                                       --LHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESA--NLTA
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                                                                                                                                       standard;
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                          (first
                                         gingivalis protein
                                                                                                                                     Protein:
                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hocking DM, Webb EA;
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Pred. No.
           periodontal disease;
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                                          PG116.
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10 - DEC-1997;
31 - DEC-1997;
30 - JAN-1998;
10 - MAR-1998;
09 - APR-1998;
23 - APR-1998;
22 - MAY-1998;
29 - JUL-1998;
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N-PSDB; AAX91554.
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                                                                                                                       205
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530 egeailitqaefmrrmrdmaqlqpqmsfyg-elpdsynlvlntdhçlidrv-lsgekesv
                                                488
                                                                                                                                                                                                                                                                57 LTCLLFSGNYEALPIIYKNGDIVRFHRLKIQVY-----KKETQGIISSGFASLTFEGTL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , BC,
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                                                                                                                                             klf----veygmltdekf--yeraakfflftdmdghkytfdeyrtlvegvqtdkdggvvy
                                                                                                                                                                   KLCDVQPMQYFDLTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVL1QDLVLE-----
                                                                                                                                                                                                                                        ltgily-----fpkiknnldl---grnkiqlycnqvyvtdevqqivpd-fltl-lhqvi
                        NOHSDVICOSE----PDDSFPSSGSVSLYEVERCQOLSATILIDHQYLERTPLCAILKQK
                                                                      --LHTKLOSMNSENOTMLSLEFHLHGGTSYGRGIRVLPESNSDVDOLKKDLESA--NLTA
                                                                                             ly atd kh gqy shvkrasd kgy svmlldgqldphiv sileqklekth fvrvdsdtinnlir\\
                                                                                                             1; Page 295-296;
                                                keeraevklsdteratlvkl-fear---
                                                                                                                                                                                                                                                                                          101;
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Rothel LJ,
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                                                                                                                                                                                                                                                                                         ; Score 99; DB 2
; Pred. No. 0.83;
69; Mismatches
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          KMYEALBYWASTHMSPSWTLLKLCDVOPMOYFDLTCOLLGKAEVDGASFLLKVWDGTRTP | :: . | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                          l Similarity 19.
91: Conservative
                                                                                                                                                        990S-0148171
990S-0148171
990S-0148341
990S-01493684
990S-0149175
990S-0149426
990S-0149723
990S-0149902
990S-0150684
990S-0151068
990S-0151068
990S-0151080
990S-0151080
990S-0151081
990S-0151381
990S-0151381
990S-0151381
990S-0155753
990S-0155753
990S-0155836
990S-0158369
990S-0159331
                                                                                           3.6%;
                                                                            62:
                                                                          Score 99; DB 2
Pred. No. 1.6;
62; Mismatches
                                                                                145;
                                                                                                                   Length 1002;
                                                                                Indels 164;
                                                                                Gaps
                                         190
                                                                                     20:
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10. JIN-1999
114. JUN-1999
116. JUN-1999
117. JUN-1999
118. JUN-1999
119. JUN-1999
120. JUN-1999
121. JUN-1999
121. JUN-1999
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124. JUN-1999
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128. JUN-1999
129. JUN-1999
129

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RESULT 1
AAB47250
AD647250
AD747250
AD7
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This sequence shows a protein containing calmodulin/calcium binding motifs which was identified using the method of the invent The method comprises a computer system for extracting information from biological sequence databases, which receives a motif that do
                                                                                                                                   Example
                                                                                                                                                                              New Caenorhabditis elegans mitochondrial calcium-binding protein p95.5/YN52, identified by protein motif database searching, usefor regulating intracellular calcium ions and in drug screening assa;
                                                                                                                                                                                                                                                                                         WPI; 2001-308615/32.
N-PSDB; AAC85804.
                                                                                                                                                                                                                                                                                                                                                                     Murphy AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999; 99US-0427867
26-OCT-1999; 99US-0427895
97-SEP-2000; 2000US-0657253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrial calcium-binding protein; p95.6/YN52; calcium: drug screening; sequence extraction; PP7; calcium binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                  (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-001-2000; 2000WO-US29787
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                                                                                                                                   Fig 13;
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                                                                                                                                                                                                                                                                                                                                                            Clevenger
                                                                                                                                                                              drug screening assays
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a desired polypeptide sequence. The computer searches the database based on a query formulated from the motif to obtain a set of polypeptide sequences which are then filtered and a report of the filtered set of polypeptide sequence information is then displayed. The computer system is useful for identifying recombinant C.elegans p95.5/NN52 and other mitochondrial proteins involved in binding, transport or other regulation of intracellular calcium which provides targets for screening assays that identify agents capable of altering a mitochondrial activity.
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     437
                                  410 DVKL 413
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                                                                                             QOYRIRAKLRSY--KPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIF-----QDGATKTP
                                                                                                                                   VSLYEVERCQQLSATILTDHQYLE----
                                                                                                                                                                                           nllhrwernkmksvlipptetnrdhdtdskh-nkvgvtfnahgriktngspteh-----
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                                                                                                                                                                                                                                                                                          SLKVG---SFLRIYSLHTK--LQSMNS------ENQTMLSLEFHLHGGTSYGRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKYFNFTTED-----HKMVEALR----VWASTHMSPSWTLLKLCDVQ------PMQYFDLTC-
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                                                                                                                                                                                                                                                                                                                                                                                                                      -----QLLGKAEVDGASFLLKVWDGTRTPF-------PSWRVLI------QD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 98.5; I
; Pred. No. 0.86
51; Mismatches
                                                               ---yeichdgkvvtifsasnyyeegsnrga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118;
                                                                                                                                                              -RTPLCAI - - - LKQKAP
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Search completed: April 9, 2002, 17:08:16 Job time: 595 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassifie
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1776
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                                                                                    sp_organelle:*
sp_phage:*
                     sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_mammal:*
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     sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•						•
 -	1660	93.5	634	4	Q9NW19	Q9nw19 homo sapien
2	1650	93.5	524	4	Q9NUX5	homo
w	34 B	19.6	384	4	Q9Н662	homo
4.	324	18.2	113	11	Q9CYS7	Q9cys7 mus musculi
ı,	57.5	9.4	555	w	013988	013988 schizosacch
תי	153	8.6	463	10	Q9FNH7	09fnh7 arabidopsi
7	144	8.1	497	Ŋ	076380	076380 oxytricha 1
ထ	130	7.3	251	ഗ	045595	045595 caenorhabdi
ည	111	5.2	759	w	Q9C2K8	Q9c2k8 neurospora
10	109	5.1	587	Ŋ	093702	Q93702 caenorhabd
11	103	ა. დ	1044	4	Q9Y4E4	Q9y4e4 homo sapie:
12 1	102.5	ري 00	4370	4	Q9H3V5	Q9h3v5 homo sapien
_	00.5	5.7	215	ഗ	09XWB2	Q9x≈b2 caenorhabdi
14	98	5.5	1198	10	004538	004538 arabidopsis
15	96	5.4	632	S	015742	015742 dictyosteli
16	20	5.4	752	Ŋ	Q9GUX3	Q9gux3 dictyostel
17	95.5	5.4	474	10	049474	049474 arabidopsis
18	94.5	5.3	442	ر. ري	Q9VJU1	09∵jul drosophila
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8 Q9TBZ8	09C2X7	10 09M2Z1	.0 Q9SJ37	0 09SNK7		Q9CM28	.0 Q9MAU9	3 Q9W6V5	2 053127	_	3 Q9IB98	_	1 P97412		_		083436		015628		09CI25	0 Q9C9U5	09нрр8	10 Q9LS89	_	
Q9tbz8 greya punct	Q9c2x7 candida alb	Q9m2zl arabidopsis	Q9sj37 arabidopsis	Q9snk7 oryza sativ	Q9g4l4 phytomyza i	Q9cm28 pasteurella	Q9mau9 arabidopsis	Q9w6v5 gallus gall	053127 mycobacteri	Q9hfk5 neurospora	. Q9ib98 potamotrygo	097699 bos taurus	P97412 mus musculu	Q9xv62 caenorhabdi	Q9ttk4 bos taurus		083436 treponema p	Q9sgv4 arabidopsis	016628 caenorhabdi	O9lnx9 arabidopsis	Q9ci25 lactococcus	Q9c9u5 arabidopsis	Q9hpp8 halobacteri	Q91s89 arabidopsis	Q9hkq3 thermoplasm	

ALIGNMENTS

	O; 121 KYFNFTTEDHKMYEALRYWASTHMSPSWTLLKLCDVOPMQYFDLTCQLLGKAEVDGASFL 180	
	Db 51 LFSGNYEALPITYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPITPRTSS 120	_
	C) OF DE ORDER CONTROLLED TO THE CONTROLLED TO T	
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	Db 1 MSLVPATNYIYIPLNQLKGGIIVNVYGVVKFFKPPYLSKGTDYCSVVIIVDQTNVKLTCL 60	_
	Q; 1 MSLVPATNYIYTPLNOLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60	_
ç;	Matches 317; Conservative 2; Mismatches 2; Indels 0; Gaps	
	93.5%:	
	SO SEQUENCE 634 AA; 71425 MW; COA9C40823F9540C CRC64:	
	EMBL; AK001230; BAA91568.1;	
	submitted (FEB-2000) to the	
	RT "NEDO human cDNA sequencing project.";	
	Watanabe S., Kimura K., Murakami K.	
	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi	
	RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,	_
	RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,	_
		_
	RP SEQUENCE FROM N.A.	
		_ ~
	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	_
	Eukaryota: Metazoa; Chordata;	_
	Homo sapiens (_
	CDNA FLJ10368 FIS, CLON	_
	DI 01-0CT-2000 (ILEMBERE). 15, bast sequence update)	
	01-0CI-2000 (TrEMBLIE) 15,	
	Q9NW19;	
	ID Q9WW19 PRELIMINARY; PRT; 634 AA.	
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Matches
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.:
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai I., Ota I., Hayashi K., Sugiyama T., Otsuki I., Suzuki V., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakarnatsi Nakamura Y., Nagahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel 15, Created)
01-OCT-2000 (TrEMBLrel 15, Last sequence update)
01-JUN 2001 (TrEMBLrel 17, Last annotation update)
HYPOTHETICAL 71.4 KDA PROTEIN (UNKNOWN) (PROTEIN FOR MGC:1028:).
HOmo sapiens (Human).
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Strausberg R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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KYENETTEDHKMYEALEVWASTHMSPSWTLLKLCDVOPMOYEDLTCOLLGKAEVDGASEL
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                                                                                         KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMOYFDLTCQLLGKAEVDGASFL
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317; Conserv
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Best Local
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09CYS7;
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
2810458H16RIK PROTEIN.
2810458H16RIK
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09H662;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa;
Mammalia: Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

IISSUZ-HUMAN SMALL INTESTINE:

IISSUZ-HUMAN SMALL INTESTINE:

Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tash

Watanabe Y., Obayashi M., Nishi T., Shibahara T., Tanaka

Nakamura Y., Isogai T., Sugano S.;

"MEDO human cDNA sequencing project.";

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
CEMA: FLJ22581 FIS, CLONE HSI02573.
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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Mammalia; Eutheria;
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ilarity 94.4%;
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Catarrhini;
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SEQUENCE FPOM N.A.

Isogai T., Ota T., Hayashi K., Sugiyana T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wadatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saitc K.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saitc K.,

Wanamoto J., Wakanatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.":

"NEDO human cDNA sequencing project.":

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKOO1230; BAA31568.1;

SEDOUENCE 534 AA; 71425 MM; COA9C40823F9540C CRC64:
                                                                                                                                                                                                                       O9NW19 PRELIMINARY: PRT; 634 AA.
O9NW19:
01-OCT-2000 (ITEMBLrel. 15, Created)
01-OCT-2000 (ITEMBLrel. 15, Last sequence update)
01-OCT-2000 (ITEMBLrel. 15, Last annotation update)
CDNA FLJ10368 FIS, CLONE NIZRM2001544.
                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa: Chordata:
Mammalia; Eutheria: Primates;
NCBI_TaxID=9505;
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O9H662:
O1-MAR-2001 (TEMBLrcl. 15, Created)
O1-MAR-2001 (TEMBLrcl. 15, Last sequence update)
O1-MAR-2001 (TEMBLrcl. 16, Last annotation update)
CDMA: FLJ2281 FIS, CLOME HSIO2573.
Homo sapiens (Human).
Eukar;ota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini; Hominidae:
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Watanabe K., Kumaqai A., Itakura S., Yamazaki
suzuki Y., Obayashi M., Nishi T., Shibahara T.
Nakamura Y., Isoqai I., Sugano S.:
"NEDO human cDNA sequencing project.":
"NEDO human cDNA sequencing project.":
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AK025234; BAB15404.1:
SEQUENCE 384 AA: 43161 MW: 67C968BD595CECAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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ibahara T., T.
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Post-processing: Minimum Match 0%
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Perfect score:
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Maximum DB seg length: 200000000
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SPIREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
13: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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2732
1 MSLVPATNYIYTPLNOLKGG......HHYGTGYCTPPICVCYDLYT 519
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   sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*.
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	2637	96.5	634	4	Q9NUX5	Ognux5 homo sarien
2	2628	96.2	634	4	Q9NW19	homo san
w	1321	48.4	384	4	Q9н662	homo
4	976	35.7	317	4	095018	homo sar
υ	324	11.9	113	11	Q9CYS7	Ç3cys7 mus ⊤isculu
5	201.5	7.4	555	w	013988	017988 schizosacch
7	153.5	ა. ა.	463	10	Q9FNH7	09fnh7 arabidopsis
œ	144.5	ა. ა	497	ۍ	076380	076380 oxytricia t
Q	130	4 . 8	587	v	Q93702	Q93702 caenorhandi
10	117.5	4.3	251	ب	045595	045595 caenorhabdi
11	115	4.2	1115	12	090мн2	
12	111	4 . 1	759	w	Q9C2K8	09~2k8 neurosirra
13	110.5	4.0	483	10	Q9XE80	G9xe80 sorghin bic
14	110.5	4.0	1044	4	Q9Y4E4	Q974e4 homo sapien
15	108	4.0	1217	S	09XV62	Q9x752 caenorhabdi
15	106	3.9	2391	v	Q27732	
17	105.5	3.9	548	S	Q9NKD4	Q9nkd4 drosophila
1.9	105	ш	655	-2	Q12890	012890 homo sarien
119	101	ند) 00	1112	12	09YUR5	turker

Ouery Match Best Local Similarity

95.5%; 99.2%;

Score 2637; DB 4; Length 634; Pred. No. 1.2e-214;

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45	44	43 9	42	41	40 9	39 9	3.8 9	37	36	35	34	. 33	2	<u></u>	30	9	28 10	7	-	25 10		_	22	21 10	20 103	
97 3	97 3	7.5 3.	98	98	8.5	8.5	98.5 3.	99 3.	99 3.	99 3.	99 3.	100 3.	100.5 3.	101 3.	101 3.		101.5 3.	٦ 102	2.5	102.5 3.	2.5 3.	103 3.	103 3.	3.5	3.5 3.	
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10 098819	2 024967	12	5 Q9BJX9	5 Q17429	ري د	υī	5 Q9N8A6	5	10 Q9M2Z1	œ	2 (10	3 Q06681	10 Q9SHP2	5 Q9VJU1	2 Q99RD2	10 Q9SJI3	4 Q9H3V5	10 Q9SLM4	5 016628	13 Q9IB52	5 062239	2 Q9CGJ2	10 Q9XEJ5	2 Q9JMM8	
O9ss19 arabidopsis	024967 helicobacte	O56271 human herpe	Q9bjx9 plasmodium	Q17429 caenorhabdi	077382 plasmodium	Q9txj6 leishmania	Q9n8a6 trypanosoma	077023 drosophila	Q9m2zl arabidopsis	019880 cyanidium c	Q9s3q2 porphyromon	Q9fi77 arabidopsis	Q06681 saccharomyc	Q9shp2 arabidopsis	Q9vjul drosophila	Q99rd2 staphylococ	Q9sji3 arabidopsis	Q9h3v5 homo sapien	Q9slm4 arabidopsis	O16628 caenorhabdi	Q9ib62 xenopus lae		Q9cgj2 lactococcus	Q9xej5 zea mays (m	Q9jmm8 wolbachia s	

ALIGNMENTS

4 AA. Ce update) tion update) tion update) (PROTEIN FO Vertebrata: i; Hominidae i; Hominidae i; Hoshidae T., Otsuki uka S., Yosh k, DDBJ datab k, YDDBJ datab k, YDDBJ datab k, DDBJ datab	RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUE=SKIN, AND MELANOMA; RC TISSUE=SKIN, AND MELANOMA; RA Strausberg R.; RI Subritted (FEB-2001) to the EMBL/GenBank/DDBJ d DR EMBL; AK001935; BAA91988.1; DR EMBL; AK002580; BAB14110.1; DR EMBL; BC002923; AAH02923.1; SQ SEQUENCE 634 AA; 71441 MW; 123A12CABE708C91	[2] SEQUENCE FROM N.A. Isogai T., Ota I., Hayashi K., Sugiyama Isogai T., Ota I., Hayashi K., Sugano S., Aots Matsunawa H., Ishii S., Kawai Y., Salio Makamura Y., Nagahari K., Masuho Y. Salio Nakamura Y. Nagahari K., Masuho Y. Submitted (AUG-2000) to the EMBL/GenBan	SEQUENCE FROM N.A. IISSUE=PLACENTA: ISOGAI T., Ota T., Hayashi K., Sugiyama Isogai T., Ota T., Hayashi K., Sugano S., Aots Nishikawa T., Nagai K., Sugano S., Saito Matsunawa H., Ishii S., Kawai Y., Saito Nakamura Y., Nagahari K., Masuho Y., Sa "NEDO human cDMA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBan	O99UX5 O99UX5 O99UX5: O1-CCT-2000 (TrEMBLrel. 15, Created) O1-CCT-2000 (TrEMBLrel. 15, Last sequence) O1-UN-2001 (TrEMBLrel. 17, Last annotate) O1-JUN-2001 (TrEMBLrel. 17, Last annotate) Hypotherical 71.4 KDA PROTEIN (UNKNOWN) Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Marmalia; Eutheria; Primates; Catarrhini NCBI_TaxID=9805;
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EMBL; AK001935; BAA391988.1; -
EMBL; AK002580; BAB44110.1; -
EMBL; BC002923; AAH02923.1; -
SEQUENCE 634 AA; 71441 Max.
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Strausberg R.
Submitted (FE
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Logai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su Isogai T., Otsuki T., Su Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshiyawa Matsunawa H., Ishii S., Kawai Y., Salto K., Yamamoto J., Nakamura Y., Hagahari K., Masuho Y., Sasaki N.:

"NEDO human cDNA sequencing project.":

"NEDO human cDNA sequencing project.":
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TISSUE-PLACENTA;

TISSUE-PLA
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01-OCT-2000 (TrEMBLrel. 17, Last sequence update).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 71.4 KDA PROTEIN (UNKNOWN) (PROTEIN FCP
HOMO Sapiens (Human).
Eukharyota, Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae:
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Best Local S
Matches 633
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C 094562;
C 094562;
C 094562;
C 094562;
C 001-MAR-2001 (TrEMBLrel. 16, Last sequence update)
I 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
E CDMA: FLJ2561 FIS, CLONE HSI02573.
S HCmo sapiens (Human).
S Hcmo sapiens (Human).
C Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eu Mammalia: Eutheria: Primates: Catarrhini: Hominidae: H X NCHITTAXID-9606;
SEQUENCE FFOM N.A.
ILSSUE-HUMAN SMALL INTESTINE:
ILSSUE-HUMAN SMALL INTESTINE:
Watunabe K., Kumagai A., Itakura S., Yamazaki M., Tashi
Watunabe K., Kumagai A., Nishi T., Shibahara T., Tanaka
Nakamura Y., Isogai T., Suqano S.;
"MEDC human CDNA sequencing project.":
"MEDC human CDNA sequencing project.":
SUBL: AKO26234: BAB15404.1: -.
SEQUENCE 384 AA: 43161 MW; 6CC968D595CECAC6 CRC54;
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i: Hominidae;
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Title:
Perfect score:
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Maximum Match 1000
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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 SPIREMBL_17:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
4: sp_funga:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
12: sp_vius:*
13: sp_verteb::
14: sp_unclass
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Gapop 10.0 , Gapext 0.5
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3324
1 MSLVPAINYIYTPLNOLKGG......GTDNQICYOIFDTTVAEDVI 634
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sp_mhc:*
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sp_unclassified:*
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                                                                                                                                                                         sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	
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Result No.	Score	Query Match	Query Match Length	B G	ID	Description
	3324	100.0	3	4-	Q9WW19	Q9nw19 homo sapien
2	3317	99.8	534	4	Q9NUX5	homo
ندا	2001	60.2		4	Q9н662	omed
4	1656	49.8		4	095018	omci
رب ر	716	21.5		4	Q90G95	homo
œ.	324	9.7		11	Q9CYS7	ระเ
7	199.5	5.0		w	013988	
œ	153.5	4.5		10	Q9FNH7	Q9fnh7 arabidopsis
w	144.5	4.3		ű	076380	076380 oxytricha t
10	130.5	3 9		υ	Q93702	Q93702 caenorhabdi
11	123	3.7		12	Q9QMH2	Q9qmh2 parvo-like
12	122	3.7		10	040392	Q40392 nicotiana q
13	118	3.5	1217	ű	Q9XV62	
14	117.5	3.5	251	СI	045595	045595 caenorhabdi
15	116	3.5	1044	4-	Q9Y4E4	Q9y4e4 homo sapien
15	114.5	3.4	749	w	Q9P7X5	09p7x5 schizosacch
17	114.5	3.4	1110	10	09FI77	09fi77 arabidopsis
18	114	3.4	668	. 10	Q9SG75	Q9sq75 arabidopsis
19	-1-	٠ 4	917	10	09CAF6	

45	44	43	42	41	40	39	86	37	36	35	34	33	. 32	<u>,</u> 31	30	29	28	27	25	25	24	23	22	21	20
105	105	105.5	. 105.5	105.5	105	106	105	107	107.5	107.5	108	108.5	109	109.5	110	111	111	111.5	112==	112	112	112.5	114	114	114
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Q9YUR6	09V5N5	P95814	Q99RD2	Q9NKD4	Q9VBR8	Q9SSL9	Q9SHP2	026978	Q9C6R1	092010	031052	Q9XEJ5	Q9FZK7	Q9ZT94	Q9CGJ2	Q9SXQ3	Q9C2K8	09XE80	Q19317	Q9SXQ5	Q9FW49	Q9SZ52	027732	09SXQ4	Q9VAD1
. Q9yur6 turkey aden	Q9v5n5 drosophila	P95814 streptomyce	Q99rd2 staphylococ	Q9nkd4 drosophila	Q9vbr8 drosophila	Q9ss19 arabidopsis	Q9shp2 arabidopsis	026978 methanobact	Q9c6rl arabidopsis	Q9zuiO arabidopsis	O31052 streptococc	Q9xej5 zea mays (m	Q9fzk7 arabidopsis	Q9zt94 arabidopsis	Q9cgj2 lactococcus	Q9sxq3 arabidopsis	Q9c2k8 neurospora	Q9xe80 sorghum bic	Q19317 caenorhabdi	Q9sxq5 arabidopsis	Q9fw49 arabidopsis	Q9sz52 arabidopsis	Q27732 plasmodium	Q9sxq4 arabidopsis	Q9vad1 drosophila

ALIGNMENTS

RESULI	TLT 1
Q9NW19	19
ID	Q9NW19 PRELIMINARY; PRT; 634 AA.
AC	
DT	2000 (TrEMBLiel.
DI	(TrEMBLrel. 15,
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE	E NI
SO	Homo sapiens (Human).
ጸ	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
8	Catarrhini; Hominidae;
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RN	[1]
RР	SEQUENCE FROM N.A.
RA	
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA	Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA	M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA	Ninomiya K., Iwayanagi T.;
R1	"NEDO human cDNA sequencing project.";
RL	Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AK001230; BAA91568.1;
SQ	SEQUENCE 634 AA; 71425 MW; COA9C40823F9540C CRC64;
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3 (D	Local Similarity 100.0%; Pred. No. 1.1e-265; es 534; Conservative 0; Mismatches 0; Indels
Οy	1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60
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5	1 SOLVENIMILITE EMPERAGELLYMYLGYVARER REEL EGAGLELCGYVILLYEPGIMYADLICE GO
Qy:	51 LFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPRTSS 120
7	AT TERCHAPEN DITAK NGDIVERHERIK TOAVKKETOGITEGEREKT TERGETIGIETIGITETEN 120
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DЪ	121 KYFNFTTEDHKMVEÄLRVWÄSTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL 180

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is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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Copyright (c) 1993 - 2000 Compugen
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sp_virus:*
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sp_unclassified:*
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   2002, 08:33:16 ; Search time 22.44 Seconds (without alignments) 710.503 Million cell updates/sec
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095330 homo sarien
09b37 homo sapien
09p113 homo sapien
09y282 homo sapien
09y282 homo sapien
09lnx9 arabidopsis
09kbf1 bacillus ha
09kbf1 bucinera ap
045329 cowdria rum
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99nux5 homo sapien
09crs7 mus musculu
213998 schizosacch
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C9sj37 arabidogsis
99r119 cryptospor1
99c2k8 neurospora
09cqe7 mus musculu
095330 homo sapien
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279	251	598	313	284	2867	576	279	801	664	490	1175	518	497	490	877	306	792	1124	812	885	467	383	313	313	287
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Q9RG44	Q9ZEY5	Q9YW15	Q9AKC5	O9AFA1	Q9N2M3	09LYR8	Q9PUS5	Q9P3W3	Q9URD2	Q22200	Q47955	P91345	Q9K3R9	017840	Q99BV2	Q9KF99	Q9HG45	Q9нкQ3	Q9RT53	092007	034798	P74756	Q9AKH3	Q9AKM8	Q9R425
streptoc		Q9yw15 melanoplus	-	Q9afal cowdria rum	Q9n2m3 plasmodium		S					P91345 caenorhabdi		017840 caenorhabdi	2 baboon	Q9kf99 bacillus ha			deinococcus	7 arabidops	bacillus s			akm8 ricketts	Q9r425 cowdria rum

ALIGNMENTS

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RESULT
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Matches 109
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EMBL: AKO01330: BAA91568.1: -. COA9C40823F9540C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09Nw19;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxTD=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60
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Pred. No. 1.1e-51;
Mismatches 0;
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Submitted (FEB-2001) to the E
EMBL; AK001935: BAA91988.1: -
EMBL; AK022580: BAB14110.1: -
EMBL; BC002922: AAH02923.1: -
SEQUENCE 634 AA: 71441 MW;
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            STRAIN-C57BL/6J: TISSUE-EMBRYO:
MEDLIKE-21085650: pubmed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M.,
Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., F
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yam
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,
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01-JUN-2001 (TremBLrel.
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2810458H15RIK PROTEIN.
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Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki H.;
"NEDO human cDNA sequencing project.";
Submitted (#FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                               Eukaryota: Metazoa: Mammalia; Eutheria:
                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                      NCBI_TaxID=10090;
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 17, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 71.4 KDA PROTEIN (UNKNOWN) (PROTEIN FOR MGC:10280).
HOMO Sepiens (Human).
Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleosteni:
Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Homo.
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09: Conservative
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                                                                                                                                                                                                                                                                                              (Mouse)
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                                                                                                                                                                                                                                               Chordata;
Rodentia;
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Last annotation update)
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Pred. No. 1.1e-51;
Mismatches 0;
                                                                                                                                                                                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Aotsuka S., Yoshikawa
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                                         Yamanaka
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                                                                   . Ishii
Fukuda
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Best Local S
Matches 31
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Best Local S
Matches 63
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013988:
01-JAN-1599
01-MAY-2000
01-MAY-2000
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Hypotherical
SEQUENCE 55
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHELLCAL 64.1 KDA PROTEIN C26H5.06 IN CHROMOSOME
SPACE:6H5.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Flettcher C., Fijita M., Gariboldi M., Lee N.H., Lyons P., Harchionni L., Mashima J., Mazzarelli J., Mombaerts P., Rodone P., Fing B., Ringwald M., Rodriguez I., Sakamoto N., Rossaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki B., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Poris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Unarachia-yi Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Tunctional annotation of a full
"Tunctional annotation of a full
"Auture 409:685-690(2001).
EMBL: AK013364: BAB28810.1: -.
MGD: K31:1990085: 2810458H15Rik.
SEQUENCE 113 AA: 12740 MW: (
                                                                                                                                                                                                                                                                                                            Oliver K., Harris D., Barrell B.G., Rajandream Submitted (SEP-1997) to the EMBL/GenBank/DDBJ c EMBL; Z33125; CAB15192.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast). Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes
                                                                                                                                                                                                                                                                                                                                                            STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces
NCBI_TaxID=4896;
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                                                                                                                               KKWIIVNLEGIVKDETPSROSLHGTKDWVTTVYLWDPTCDTSSIGLQIHLESKQGNDLPV
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                                                                 IKOVGOPLELHOITLRSYRDRTOGLSKDQF
                                                                                                                                                              KGGTIVNVYGVVKFFKPPYLS-KGT-DYCSVVTIVDQT----NVKLTCLLFSGNYEALPI
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                                                                                              IYENGDIVEFHELKIQVYKKETOGITSSGF
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                                                                                                                                                                                                l Similarity
31: Conser
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73.3%;
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Pred. No. 7.2e
6; Mismatches
                                                                                                                                                                                            Score 114; DB 3;
Pred. No. 0.00074;
B; Mismatches 35
                                                                                                                                                                                                                                                                               A79DAA95A0C4F803 CRC64;
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                                                                                                                                                                                                                             Length 555
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PRELIMINARY:

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Bést Local S
Matches 31
                                                                                                                                         Overy Match
Best Local Similarity
                                                                                                                    Matches
                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBLA;

MEDLINE-20083487; Pubmed-10517197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Sorerville C.P.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome II of Arabidopsis thaliana.";

Nature 402:761-789(1999),

EMBL; AC007018; AAD29059.1;

SEQUENCE 318 AA. 35220 MW; EFFIADA077B93AZE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9SJ37:
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, AT2G05210 FROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta: Tracheophyta:
Spermatophyta; Magnolicphyta: eudicotyledons; core eudicots; Rosidae:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota: Alveolata: Ciliophora: hypotrichs: Stichotrichida:
Oxytrichidae: Oxytricha.
NCBI_TaxID-5945:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBL.cl. 08, Created) 01-NOV-1998 (TrEMBL.cl. 08, Last sequence up 01-UN-2001 (TrEMBL.cl. 17, Last annotation ALPHA TELOMERE BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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01-NOV-1998
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24
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VSLIGIVLEOREPROCRNNDWICTLRIIDDIYFSFGLIVNVFSKTLEOLFOIKNHDDMIL 83
                                                  VNVYGVVKFFKPPYLSKGIDYCSVVTIVDQI--NVKLTCLLFSGNYEALPIIYKNGDIVR 80
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                                                                                                                                            15.0%;
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                                                                                                           Score 85; DB |
Pred. No. 0.45
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 0.0046;
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Q9Y119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBI/GenBank/DDBJ databases EMBL; AF132307; AAD42052.1; -...
InterPro: IPR0000909; PI_PLC_X.
PROSITE: PS500007; PIPLC_X_DDMAIN; 1.
SEQUENCE 473 AA: 53997 MN: DEC281A982343878 CRC64;
                                                                                              German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/
EMBL; AL513442; "AC286431; -
SEQUENCE 759 AA; 85218 MW; DO
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Fungi: Ascomycol
Sordariales: Scrdariaceae:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
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13.2%;
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Pred. No. 4.4;
Pred. Mismatches
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                        Length 759;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fikuda S.,
RA Aizawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Onackeni Sh. J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Onackeni Sh. J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Onackeni Sh. J.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Wasilo T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee S.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee S.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch F.-F.,
RA Suzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker T., Willing L.,
RA Havashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kchtsuki S.,
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Best Local Similarity
Matches 19; Conserv
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 095330;
01-MAY-1999
01-MAY-1999
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STRAIN=C57BL/6J; TISSUE=EMBEYONIC |
MEDLINE=21085690: PubMed-11217851;
MEDLINE=21085690: PubMed-11217874 K.
                                                                                                                                                                                                                                                                                                                                                                      *Functional annotation of a full-length mouse cDNA collection Nature 409:585-590(2001).

EMBL: AK013942: BABE29073.1: -.

EMBL: AK0039350: BABE29073.1: -.

MGD: MGI:1913516: 2310915B14Rik.

SEQUENCE 383 AA; 43208 MW; 97EF08712201E0C2 CRC61:
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Eukaryota: Metazoa; Chordata:
Mammalia: Eutheria; Podentia:
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Last sequence update)
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Pred. No. 7.2;
21; Mismatches
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Sciurognathi; Muridae; Murinae; Vis.
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Best Local Similarity 25.2
Matches 17: Conservative
                                                  09F1L3;
09F1L3;
01-001-2000;
01-001-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BCN7 PPELIMINARY: PRT: 228 AA.
Q9BCN7:
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Full insert sequence of mapped XREF EST
Submitted (AUG-1998) to the EMBL/GenBank
EMBL: AF091085; AAC72954.1; -.
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Mammalia: Eutheria; Primates;
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Mammalia; Eutheria; Primates;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 HLSFGEDYFGIVNPLDHINVTAPQASMNFOYFVKVVPTVYNKVDGEVLRINQFSVTRHEK 170
                                                                                                                                                                                                                                                                                                                                                                                                                    139 HLSEGEDYPGIVHPLDHINVTAFQASMMFQYFVKVVPTVYMKVDGEVLRTNQESVTRHEK 198
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                                                                                                                                                                                                                                                                                                            199 VANGL 203
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17; Conserv
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                                                  (TrEMBLrel, 15, (TrEMBLrel, 15, (TrEMBLrel, 15,
                                                                                                                                                                      PRELIMINARY:
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25.2%;
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                                                        Created)
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Last annotation updat
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74; DB .
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 17
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Best Local S
Matches 17
                                                                                                                                                                                                                                                   Submitted (NOV-2000) to the EMBL; AF151812; AAD34049.1; EMBL; AF077030; AAD27763.1; EMBL; AL121586; CABB9412.1; SEQUENCE 383 AA; 43222 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Zhang J., Liu T., Ye M., Zhang Q., Fu G., Zhou Zhang J., Liu T., Ye M., Chen Z.;

"Human hypothetical 43.2 Kd protein.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
Lin W.-C.
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01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
CGI-54 PROTEIN (DJ47704.2) (CGI-54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative gene cloning: Identification of novel Caenorhabditis elegans proteome as template."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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Zhang C., Yu Y., Zhang
Liu M., He F.;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                           HLSFGEDYPGIVNPLDHINVIAFQASMMFQYFVKVVPIVYMKVDGEVLRINGFSVIPHSK
                                                                                  YLSKGTDYCSVVTIVDQINVKL--TCLLFSGNYEALPIIYK--NGDIVRFHRLKIÇTYKK
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                                                                                                                                        l Similarity
17; Conser
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17: Conser
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43222 MW;
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                                                                                                                                                           13.1%;
26.2%;
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                                                                                                                                   Score 74: DB
Pred. No. 8.1:
18: Mismatches
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Pred. No. 7.2;
LB; Mismatches
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7.2;
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Best Local
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031NX9:
01-737-2000 (IrEMBLrel. 15, Created)
01-737-2000 (IrEMBLrel. 15, Last sequence update)
01-739-2001 (IrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J.R.
Submitted
                                                                                                                                                          Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kha C., Altafi H., Bei Q., Chin*C., Chiou J., Choi E., Conn L., Kim C., Gonzales A., Hensen N., Howing B., Koo T., Lam B., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Lenz G., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Falm C., Fham P., Sakano H., Schwartz J., Southwick A., Thaveri Torinin M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukar;ota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales: Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukar;ota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pter;oota: Necptera; Endopteryota: Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
WCB1_Tax1D=7227;
                                                              Submitted
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mottier, Cadieu, Dreano, Lelaure, Galibert F.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
SECTENCE FROM N.A
                                                SEQUERY'E FROM
                                                                                               SEQUENCE FROM
                                                                                                                        Sub-1: ted (FEB-2000)
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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                                                                                                                                                sequence
                       (MAR-2000)
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                                               N.A.
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Pred. No. 8.8;
14; Mismatches
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RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., RA Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., RA Theologis A., Ecker J.;
RI Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Cc. :- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR InterPro: IPR003592; LERP. DR InterPro: IPR003592; LERP. DR InterPro: IPR003592; LERP. DR InterPro: IPR003592; LERP. DR InterPro: IPR003592; LERP. DR Fam: PF00959; pkinase: 1.
DR FAMT: FM002290; Ser_thr_kin_actsite.
DR FAMT: SM0021; STYCE: 1.
DR PROSITE: PS00107: PF0TEIN_KINASE_DOM: 1.
DR PROSITE: PS00107: PF0TEIN_KINASE_DOM: 1.
DR PROSITE: PS00107: PF0TEIN_KINASE_DOM: 1.
DR PROSITE: PS00108: PROTEIN_KINASE_ST: 1.
DR PROSITE: PS00108: Serine/chreonine-protein kinase: Transferase.
SO SEQUENCE 937 AA: 104477 MW: 98A7D8A6FC808C62 CRC64:
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Search completed: April 12, 2002, 08:34:28 Job time: 72 sec
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Best Local Similarity 24.5%; Pred. No. 33;
Matches 29; Conservative 15; Mismatches
                                                                                                                                                                                                                                              152 LRYFEDGVRNCYTLIVIOGINYLIVAMFTYGNYDNLNTHPKFDLYLGPNIWTTVDLOR 209
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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567
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Com
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/cgn2_5/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_5/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_5/ptodata/2/iaa/PCTUS_COMB.pep:*
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    DВ
  US-08-733-230-2
US-08-95-3-95-2
US-08-95-1-134-2
US-08-645-193B-15
US-08-162-0728-1
US-08-162-0728-1
US-08-162-0728-4
US-08-162-0728-4
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US-08-162-1-290-5
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US-08-17-188-9
US-08-413-118-9
US-08-413-118-9
US-08-413-118-9
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US-08-413-118-9
US-08-349-006-2
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Sequence 15, Appl
Sequence 18, Appli
Sequence 20, Appli
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US-08-733-230-2
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Query Match 12.4
Best Local Similarity 30.3
Matches 27: Conservative
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APPLICANT:
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56.5 10.0 907 3 US-08-720-229-19 56.5 10.0 907 5 PCT-US94-04180-2 56 9.9 331 2 US-08-878-989-21 56 9.9 331 3 US-09-101-146-64 56 9.9 331 3 US-09-101-146-64 56 9.9 863 4 US-09-727-995-21 56 9.9 863 4 US-09-738-903-11 55.5 9.8 592 3 US-08-918-133-2 54.5 9.6 251 1 US-08-425-336-100 54.5 9.6 251 1 US-08-425-336-101 54.5 9.6 251 1 US-08-448-1138-101 54.5 9.6 251 1 US-08-448-1138-101 54.5 9.6 251 1 US-08-488-1138-101 54.5 9.6 251 1 US-08-488-1138-101 54.5 9.6 251 1 US-08-488-1138-101 54.5 9.6 251 1 US-08-488-138-101 54.5 9.6 251 1 US-08-488-1036-100 54.5 9.6 251 2 US-08-646-360-101
0.0 907 3 U.0 907 5 P.0 90
3 0 0 2 2 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 1 1 1 0 0 0 0 0 1 1 1 0 0 0 0 0 1 1 1 0 0 0 0 0 1 1 0
US-08-720-729-19 PCT-US94-04180-2 US-08-879-989-21 US-09-101-146-64 US-09-272-795-21 US-09-272-795-21 US-09-278-303-11 US-08-991-813-2 US-08-991-813-2 US-08-991-813-2 US-08-488-1138-100 US-08-488-1138-100 US-08-488-1138-100 US-08-488-1138-100 US-08-488-1138-100 US-08-488-138-100

ALIGNMENTS

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: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-733-230-2
                                                   TELEPHONE: 352-375-8100
TELEPAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY. 110-247
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
FILING DATE:
CLASSIFICATION: 514
AITORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,95
REFERENCE/DOSKET HUMBER: UF-167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-88000
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2421 N.W. 41St CITY: Gainesville SIATE: FL COUNTRY: USA ZIP: 32606 COMPOUTER READABLE FORM: MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Rucleic Acid Vaccines Aga
TITLE OF INVENTION: Rickettsial Diseases and
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, Application US/08733230
o. 6025338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ganta, Roman Reddy
McGuire, Travis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mahan, Suman M
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12.4%;

Score 70.5; DB Fred. No. 0.47; Mismatches

Length 287; Indels

19:

18; ω --

25;

Gaps

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CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1995-10-17

NUMBER OF SEO ID NOS: 24

SOFTWARE: Patentin Ver. 2.0

SEO ID NO 2

LENGTH: 287

TYPE: PPT

ORGANISM: Cowdria ruminantium

US-08-953-325-2
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                                                                                                                                                                                                                                             Sequence 2, Application US/08741134
Patent No. 5861498
GENERAL INFORMATION:
APPLICANI: Litwack, Gerald
APPLICANI: Alnemri, Emad S.
APPLICANI: Fernandes Alnemri, I
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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANI: Barbet, Antho
APPLICANI: Ganta, Roman
                                                                                                                                     TITLE OF INVENTION: IMM
TITLE OF INVENTION: AND
TITLE OF INVENTION: METI-
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases TITLE OF INVENTION: Animals and Humans FILE REFERENCE: UF-167Cl
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 PYVCAGIGID---LVSVINATNEKLSYOGKLGISYSINSEA--SIFIGG---HFHRVIGW 245
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                                                            STATE:
                                                                             STREET: One Liberty Place CITY: Philadelphia
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                                        COUNTRY:
                                                                                                                        ADDRESSEE:
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                                                       Pennsylvania
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                                                                                                 Woodcock Washburn Kurtz Mackiewicz & No.
ne Liberty Place - 45th floor
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                                                                                                                                                                                    AND METHODS OF USING THE
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IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
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Best Local Similarity
Matches 19: Conserve
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: MOLECULE TYPE: protein
US-08-741-134-2
NAME: ESMOND, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELECHYNE: (202) 371-2540
TELECAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Patent No. 5
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kupke, Thomas
APPLICANI: Gotz, Friedrich
APPLICANI: Wempter. Christoph
APPLICANI: Jung, Gunther
ITILE OF INVENTION: Oxidative Decarboxylation of Peptides
TITILE OF INVENTION: Catalyzed by Flavoprotein EpiD
HUMBER OF SEQUENCES: 70
                                                                                                                              APPLICATION NUMBER: US/00
FILING DATE: 13-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215,568-3100
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APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
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OPERATING SYSTEM: Windows 3.11
SOFTWARE: Wordberfect for Windows 6.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                SIREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 KPPYLSKG------TDYCSVVTIVDQTNVKLTCLLFSGNYEALP--IIYKNGDIVRF 81
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COMPUTER: I
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; Pred. No. 4.6;
9; Mismatches
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US-08-162-402B-18
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 Query Match
Best Local S
Matches 24
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Matches 28; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,402B
FILING DATE: 03-DEC-1993
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFOFMATION:
TELEPHONE: 213-522-7700
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,
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PRIOR APPLICATION DATA:
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LENGTH: 990 amino acids
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 Local Similarity hes 24: Conserv
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CITY: Los Angeles
STATE: CA
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STRANDEDNESS: sit
TOPOLOGY: not re
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ilarity 29.3%;
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46 KDALTON HUMAN MILK FAT
GLOBULE (HMFG) ANTIGEN, F
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12; Mismatches
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                 Score 61.5: D
Pred. No. 2.9:
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19;
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US-08-392-625-20
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TELEFAX: (20z) ...
INFORMATION FOR SEO ID NO: 20:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
OFFIGIH: 990 amino acids
                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                           NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 30-APR-1992
AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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51 DQINVKLICLLFSGNY-----EALPITYKNG------DIVRF 81
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                                                                 4 VPAT------HYIYTPLNQLKGGTIVNVYGVVK-----FFKPPYLSKGTDYCSVVTIV 50
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                                                                                                     Conservative
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Jung, G nther
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Klein, Cora
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US-08-466-961A-20
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Best Local Sim
Matches 25;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:

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LENGTH: 990 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0652.0980004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-0CT 1991
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Pobert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                              734 IPKTYODNE IODYLLPFITELKVNNFINKFFYIKFKEDEDFIKLRLLRECEDYSQIYSFI 79:
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TITLE OF INVENTION: Biosynthetic Process for the Preparation
TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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51 DQINVKLTCLLESGHY-----EALPIIYKNG-----DIVRF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: am TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0
FILING DATE: 22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington STATE: D.C.
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                                                                                                                                 4 VPAT-----NYIYTPLNOLKGGTIVNVYGVVK-----FFKPPYLSKGTDYCSVVTIV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 990 amino acids amino acid
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Engelke, Germar
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Jung, G nther
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Schnell, No. 5843709bert
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                                                                                                                                                                                                                                                10.6%; Score 60; DB 24.5%; Pred. No. 59;
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RESULT 9
US-08-446-822-4
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MOLECULE TYPE: protein
US-07-996-772A-4
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US-07-996-772A-4
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                                                                                                                                                                           Sequence 4, Application US/08446822 Patent No. 5765879
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Best Local Similarity
Matches 23; Conserv
APPLICANT: SYNAPTIC PHARMACEUTIC/
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: AND USES THEI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
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                                                                                                                                                     GENERAL INFORMATION:
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa A.
APPLICANT: Branchek, Richard I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN TITLE OF INVENTION: RECEPTORS AND USES THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,
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                                                                                                                                                                                                                                                                                                                                          59 -CLLESGNYEAL---PITYKN 75
                                                                                                                                                                                                                                                                                                                                                                                  55 THYFIVSLAFADLLVSVLVNAFGAIELVODIWF-YGEMFCLVRTSLD---VLLTTASIFH 110
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CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                            SYNAPTIC PHARMACEUTICAL CORPORATION
VENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
VENTION: AND USES THEREOF
EQUENCES: 15
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CITY: NEW YORK
STATE: NEW YORK
SIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d

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GENERAL INFORMATION:
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Best Local S
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INFORMATION FOR SEQ ID NO: 4:
NFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FOPM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC -DOS/MS-DOS
COTTABLE: PC-TOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTOFS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                REFERENCE/DOCKET NUMBER: 42567-A-PCT/JPW/TEP TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550
TELEPHONE: (212) 654-9525
TELERA: (212) 654-9525
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 LCCLSLDRYYAICCOPLVYRN 131
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                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 -CLLFSGNYEAL---PIIYKN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 INYFIVSLAFADLLVSVLVNAFGAIELVODIWF-YGEMFCLVRTSLD---VLLI ASIFH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TNYIYTPL--NQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLT ----- 58
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23; Conserv
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amino acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                              28,678
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                                                                                                TOPOLOGY: un;
MOLECULE TYPE:
US-08-480-229C-5
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Best Local Similarity
Matches 23: Conserv
Matches
                    Query Match
Best Local Similarity
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TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 405 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Quertermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Zupancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEFHONE: (212) 790-9090 TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Poissant, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   SEQUENCE CHARACTEPISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/480,229C FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 A:enue of the Americas
CITY: New York
STATE: New York
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                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462 REFERENCE/DOCKET NUMBER: 890
                                                                                                                                                                                                LENGIH:
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                                                                                                                                                                             : 85 amino acids amino acid
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    Conservative
                                                                                                                                         unknown
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                  10.2%; Score 58; DB 2; Length 85; 30.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
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  10: Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                        8907-0026-999
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      24; Indels
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      8
      Gaps
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29 YYFFKPPYISKGIDYCSVVTIVDQTNVKLTCLLFSGNYEALPIIYK---NGDIVRFHRLK 85

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27 VKSYKVDISSNGEDWIXXTLKGDNKH-----LVFTGNTDATDVVYRPFSKPVITRFVRLR 81

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RESULT 13
US-08-542-921-2
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                                                                                                                                                                                                                             Sequence 2,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 18;
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Best Local Similarity
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TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Zupancic,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                        APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: ARAI, SATOSHI
APPLICANT: NIIZEKI, MASATSUGU
APPLICANT: MIYAKE, TOSHIRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: OFFICIALS STRAIN AND HARMFUL
OFFICIAL OFFICIAL OFFICIAL STRAIN AND HARMFUL
OFFICIAL OFFICIAL STRAIN AND HARMFUL
OFFICIAL STRAIN AND HARMFUL
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMAPE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,4
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REFERENCE/DOCKET NUMBER: 8907-0034-999
TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES: 29
                          CORRESPONDENCE
                                             NUMBER OF SEQUENCES:
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 05-JUICLASSIFICATION: 43:
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                                                                                                                                                                                                                                                                                                                                                      VKSYKVDISSNGEDWIXXTLKGDNKH-----LVFTGNTDATDVVYRPESKPVITREVPLR 81
                                                                                                                                                                                                                                 , Application US/08542921 5736514
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Zupancic, Thomas J.
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(212) 859-8854/9741
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OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSIADT
                       ADDRESS:
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US-08-680-685-2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5834295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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          CYMPUIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUIER: IRM PC compatible
CPERAING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Pateniln Release #1.0, Version #1.30
                                                                                                                                                                                                                                                               APPLICANT: 11ZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: APAL, SATCSHI
AFPLICANT: NIIZEKI, MASATSUGU
APPLICANT: NIYAKE, TOSHIRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARNFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
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ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 1159 amino acids
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CHEFENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
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                                                                                                                              COUNTRY:
                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 276082/94
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(703) 413-2220
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Pred. No. 1.3e+02;
9; Mismatches 31
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RESULT 15
US-98-880-584-2
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: MOLECULE TYPE: protein
US-98-880-585-2
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Best Local S
Matches 23
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APPLICATION NUMBER: US/08/880,584
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOP APPLICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 13-OCT-1995
APPLICATION NUMBER: JP 275082/94
FILING DATE: 14-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version =1.20
CURRENT APPLICATION DATA:
COMPATICATION NUMBER: US/08/880,584
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: IAGAWA, MICHITO
APPLICANT: ARAI, SATOSHI
APPLICANT: NIIZEKI, MASAISUGU
APPLICANT: MIYAKE, TOSHLRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: OPGANISM CONTROLLING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CBLCN, SI
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 A---TOSGSPS 504
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 10.2%; Score 58; DB 2; Local Similarity 32.4%; Pred. No. 1.3e-02; hes 23; Conservative 9; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 TOGITSSGFAS 103
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
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NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 49-209-0
REFERENCE/DOCKET NUMBER: 49-209-0
REFERENCE/DOCKET NUMBER: 49-209-0
REFERENCE(703) 413-3000
RELEFAN: (703) 413-3220
RELEFAN: (703) 413-3220
RELEFAN: (703) 413-3220
RELEFAN: (704) 410-22:
REFERENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
TOPCIL-03Y: linear
MOLECULE TYPE: protein
US-08-880-594-2

ONEY March
Best Local Similarity 32.44: Pred. No. 1.3e+02:
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 23: Conservative 9: Mismatches 31: Indels 8: Gaps
MATCHES 31: Indels 8: Indels 9: Inde
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REGISTRATION NUMBER: 24.518
REFERENCE/DOCKET NUMBER: 49-209-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEY: 248855 OPAT UP
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids

amino acid

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/542,921

FILING DATE: 13-OCT-1995

APPLICATION NUMBER: JP 276082/94

FILING DATE: 14-OCT-1994

ATTORNEY/AGENT INFORMATION:
NAME: 0BLON, NORMAN F

FILING DATE:

APPLICATION NUMBER: US/08/880,685

23-JUN-1997

Search completed: April 12, 2002, 08:34:46 Job time: 90 sec

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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="texton:9606"
/clone="MGC:10280 IMAGE:3955573*
/tissue_type="Skin, melanotic melanoma."
/clone="texton:9606"
/db_host="hull=MGC_20"
/lab_host="hull=MGC_20"
/lab_host="hull=MGC_20
                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lum,W., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Ilongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                          be found
                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information car be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 15 Row: 9 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10434050.

Location/Qualifiers
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Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The Li.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland:
Web site:
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8 T; 776 other;

Sequence 936 BP; 6 A; 138 C; 8 G;

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    Length 936;
 Score 104.4; DB 22; Length
Pred. No. 2.4e-21;
68; Mismatches 304; Indels
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                     6; Conservative 468;
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0.8%; I
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  Query Match
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleicacide sach containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 tggtgttgtgaagttctttaagcccccatatctaagcaaaggaactgattattgctcagt
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Watch 8.0%; Score 104.4; I Local Similarity 0.8%; Pred. No. 2.4e-; es 6; Conservative 468; Mismatches
                                                                                                                                                                                                                                                                             Example 6; Page 128; 159pp; English.
                                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC
                                                                            26-JUL-2000; 2000WO-US20476.
                                                                                                     26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                      monitoring gene expression.
                                                                                                                                                                                                WPI; 2001-159728/16.
                                                                                                                                                                                                                                                   single surface
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                            tcaagtatataaaaaggagactcagggtatcaccagctctggctttgcatcttgacgtt
                                                                             378 tactgaggaccacaaaatggtagaagccttacgtgtttgggcatctactcatatgtcacc
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ID AAF58254 standard; DNA; 936
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17-MAR-2000; 2000US-0190259.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface.
                                                                                                                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                                                                                                                                      Length 936;
                                                                                                                                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                                                                    Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other
                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 104.4; DB 3
llarity 0.8%; Pred. No. 2.4e-21;
Conservative 468; Mismatches 30
                                                                                     English.
                                                                                Example 6; Page 127; 159pp;
                                                                                                                                                                                                                                      monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                           single surface
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26-JUL-2001

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oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs. The primers allow obtaining of the full-length CDNAs are present human cDNA sequences; AAH03166 to AAH13628 and AAH13631 to AAH13642 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Allaheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                      678
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                                                                                                                                                                                                      Length 866;
                                                                                                                                                                                                                              30; Indels
                                                                                                                                                                Sequence 866 BP; 254 A; 162 C; 171 G; 274 T; 5 other;
                                                                                                                                                                                                   Score 342; DB 22;
Pred. No. 3.9e-93;
0; Mismatches 30;
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                                                                                                                                                                                                   Query Match 26.3%;
Best Local Similarity 91.2%;
Matches 384; Conservative
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                                                                                                                                           the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1160 cactatgtgccattttgaaacaaaagctcctcaacaataccgcatccgagcaaaattga 1219
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                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Yang Y,
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Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                  Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5056; 10078pp; English.
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                                                               21-JAN-2000; 2000US-048B725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-065191.
,19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-073344.
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Wang Z, Wehrman T,
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                                         2000WO-US34263.
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                                                                                                                                                                                                                                                                  Zhou P,
                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                         26-DEC-2000;
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Wang J, W
Zhao QA,
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--gctctggatca 1090
                                    detection by the
                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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Otsuki T;
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                                                                                                                                                                                                         Claim 1; SEQ ID 2138; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA clone (5'-primer) SEQ ID NO:2138.
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Sugiyama T, Wakamatsı
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-HAX-2000; 2000JP-0183767.
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH1362 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13639 represent human amino acid sequences; and AAH13629 to AAH13630 represent colliges, all of which are used in the exemplification of the present invention.
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                                                                                                                                                                7; Indels
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                                                                                                        Sequence 576 BP; 167 A; 113 C; 114 G; 173 T; 9 other;
                                                                                                                                         Score 545; DB 22;
Pred. No. 1.5e-154;
0; Mismatches 7;
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Best Local Similarity 98.7%;
Matches 545; Conservative
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tull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonuclectide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
conjouncleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 5'-end
sequence and an oligonucleotide comprises a 1'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide comprises a 1'-end sequence chercation of
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH13842 tepresent human cDNA sequences; AAH3628 and
AAH06603 reavesors the human cDNA sequences; AAH3628 and
AAH06603 reavesors the human cDNA sequences.
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                          Human; primer; detection; diagnosis; antisense therapy;
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                                                                                                                                                                                                                                                           Hayashi K,
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CDNA sequence SEQ ID NO:11187
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                           EP1074617-A2
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us-09-816-248-14.rng

detection by the for the encoded 1 s defined in the specification, and of the abnormality of the proteins defined in the full-length cDNAs and/or diagnosis c full-length cDNAs and/or

2537pp + CD ROM; English SEQ ID 12760; .. 8 Claim

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence. The complementary to a polynucleotide which comprises a 1'-end sequence, and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the actection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers are also useful for the cDNAs asaily without any specialised methods. AAH13629 and AAH13633 to AAH13634 to AAH13629 and AAH3635 prepresent human anino acid sequences; and AAH13629 to AAH13620 crepresent contents and an AAH13629 to AAH13621 crepresent contents and an AAH13629 conte the present invention

Sequence 2077 BP; 657 A; 401 C; 393 G; 626 T; 0 other;

ä 180 310 300 490 540 240 430 360 480 610 420 600 Gaps tttgcatctttgacgtttgagggaactttgggagcccctatcatacctcgcacttcaagc tattttgacctgacttgtcagctcttgggcaaagcagaagtggacggagcatcatttctt ctaaaggtatgggatggcaccaggacaccatttccatcttggagagtcttaatacaagac ctctttagtggaaactatgaagcccttccaataatttataaaaatggagatattgttcgc tttgcatctttgacgtttgagggaactttgggagcccctatcatacctcgcacttcaagc tctactcatatgtcaccgtcttggacattactaaaattgtgtgatgttcagccaatgcag Length 2077; Indels 80.7%; Score 1048; DB 22; 90.8%; Pred. No. 3.2e-306; live 0; Mismatches 0; Conservative Best Local Similarity Matches 1178; Conserv Query Match 191 251 181 311 241 371 61 121 431 361 491 (21 551 181 541 301 g ç g g δ g ò g õ g 9 g ò ò ò οy ò g ô

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                   cttcgtcctccaggctggagttcagtggcacggtctcggctcattgcagcctccacctcc
                                                      gtatcattatacgaggtagaaagatgtcaacagctatctgctacaatacttacagatcat
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 328)

Oian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Qu,J., Song,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu Homo sapiens cDNA clone

Unpublished (2000)
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Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 16-21-50801922
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/db_xref="taxon:9606"
/clone="GLCEVD06"
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AVESSE27 GLC Homo sapiens cDNA clone GLCEVD06 3', mRNA sequence.
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20.6%; Score 268; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.4e-58;
Matches 268; Conservative 0; Mismatches 0;
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Search completed: April 9, 2002, 22:13:58 Job time: 8873 sec

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pBluescript KS+); Site_l: BamHI; Site_2: Sall-XhoI (gtcgag j: Oligo-dr primed using primer 5'-TTTITITITITITIVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.*

197 c 205 g 299 t 1 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (Dases 1 to 341)
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA librar;
Nature Genet. 4, 373-380 (1993)
94004965
Contact: Kerlavage, AR
Bioinformatics
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EST95690 Testis I Homo sapiens cDNA 5' end, mRNA sequence.
AA382297.1 GI:2034796
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                                                                                                                                                                         Score 317.2; DB 11; Length
Pred. No. 3.5e-70;
0; Mismatches 78; Indels
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Matches 443; Conservative
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Hus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 565)
Rargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carterr,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse 15K CDNA clone set Unpublished (2001)
Other_ESTS: H3158E09-3
Contact: George J. Kargul .
Cantact: George J. Kargul .
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 1912 Medical Center Drive, Rockville, MD 20850 USA 1918 0599056 Fax: 3018659423 Email: arkerlav@tigr.org Email: arkerlav@tigr.org information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG088861 565 bp mRNA EST
H3188E09-5 NIA Mouse 15K cDNA Clone Set Mus
H3158E09 5', mRNA sequence.
BG088861.1 GI:12571425
                                                                                                                                                                                1.341
/organism="Homo sapiens"
/db_xref="ATCC (inhost):186770"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Testis I"
/sex="male"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                         /note="Organ: testis; Vector:
EcoRI; Site_2: XhoI"
68 c 67 g 98 t
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Try human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,R., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Upublished (2000)
                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
Ota.T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Makamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takao Isogai
Genomics Laboratory
Genomics Laboratory
Genomics Laboratory
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
Fax: 81-438-52-3952
Exail: genomics@hi.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
61 acaattgtcaatgtctatggtgttgtgaagttctttaagccccatatctaagcaaagga 120
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A0124189 NT2RM2 Homo sapiens cDNA clone NT2RM2001805 5', mRNA
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                                         Ouery Match
26.3%; Score 342; DB 10;
Best Local Similarity 91.2%; Pred. No. 1.7e-76;
Matches 384; Conservative 0; Mismatches 30;
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/cell_type="teratocarcinoma"
/cell_line="NT2"
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AU124189.1 GI:10948905
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHLJ9W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybrighization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 4)

RCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

A. Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@lmage.llnl.gov) for further information.

Seq primer: -400P from Gibco

High quality sequence stop: 403.
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/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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I (bases 1 to 429)

Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library

Nature Genet. 4, 373-380 (1993)
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end, mRNA sequence
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                                                                                           5:
                                                                        Score 522.4; DB 10; Length 854; Pred. No. 2.2e-122;
                                      others
                                                                                           Indels
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ESTS5213 Infant brain Homo sapiens CDNA 5' e
AA351459.1 GI:2003779
                                                                40.2%; Score 99.3%; Pred. No. 2.2. 99.3%; O; Mismatches
/clone."PLACE1005026"
/clone_llb."PLACE1"
/tissue_type="placenta"
/note="vector: pME18FE13"
a 164 c 166 g 259 t
                                    259
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Contact: Kerlavage, AR
Bioinformatics
                                                                                  al Similarity 99.3 545; Conservative
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TTCTAAAGG 680
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 19619056 Fea: 3018699058 Emel: 3018699423 Email: arkerlav@tigr.org Email: arkerlav@tigr.org information related to this EST, please check the TIGR Human Gene Information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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AL520360
                                                                                                        Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 782)
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TCGGG 1
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BASE COUNT
ORIGIN
       ORGANISM
                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 2 kb. Library constructed by Life
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                                                 Score 611.2; DB 11;
Pred. No. 5.8e-145;
                                                             Mismatches
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BF027455
BF027455.1 GI:10735167
EST.
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205 c
                                                tch 47.1%; sl Similarity 94.0%; 679; Conservative
                                                       Local Similarity
                        271
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VERSION
KEYWORDS
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone="IMAGE:395573"
// Clone=lib="NIH_MGC_20"
// Issue_type="melanotic melanoma"
// Iab_host="BH10B (phage-resistant)"
// Note="Organ: skin: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRi: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following Siadaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RI (Life Technologies)."
                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arc/PortD/DTP
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM830 row: e column: 14
High quality sequence start: 52
High quality sequence stop: 746.
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                    Euteleostomi;
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1 (bases 1 to 920)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Pred. No. 4.9e-129;
0; Mismatches 44;
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Best Local Similarity 92.0
Matches 702; Conservative
Homo sapiens
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EARLIER FILING DATE: 1997-05-29
NUMBER OF SEO ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 3
LENGTH: 12565
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                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-345-217-3
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APPLICANT: Hendrickson, Eric
APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
FILE REFERENCE: B0877/7017/HK
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
NUMBER OF SED ID NOS: 35
SOFTWARE: FastSED for Windows Version 3.0
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Sequence Application US/09345217

Patent No. 6268142

GENERAL INFORMATION:
APPLICANT: DUFF, GONDON W.
APPLICANT: CAMP, NICOLA J.
APPLICANT: DIGNOUNE, FRANCESCO S.
TITLE OF INVENTION: HITH AN IL-1 INFLAMMATORY HAPLOTYPE
FILE REPERENCE: MSA-010.02

CURRENT APPLICATION NUMBER: US/09/345,217

CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: PCT/GE98/01481

EARLIER PILING DATE: 1998-05-21

EARLIER PILING DATE: 1998-05-21
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 Length 10380;
                                       20; Indels
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Best Local Similarity 83.5%; Pred. No. 2.2e-17;
Matches 111; Conservative 0; Mismatches 20
 6.7%; Score 87; DB 4;
83.5%; Pred. No. 1.8e-17;
ative 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                        US-09-173-914-6; Sequence 6, Application US/09173914; Patent No. 6171857
 Query Match 6.7%
Best Local Similarity 83.5%
Matches 111; Conservative
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; ORGANISM: Homo Sapiens
US-09-173-914-6
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US-09-345-217-3/c
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MOLECULAR STRUCTURE OF THE HUMAN ALBUMIN GENE
IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22
OF CHROMOSOME 4
                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9206300
GENERAL INFORMATION:
APPLICANT: Hurwitz, David R
APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US92/06300
FILING DATE: 19920730
CLASSIFICATION: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Rhone-Poulenc Rorer, Inc. STREET: 500 Virginia Ave., Bldg. 3A CITY: Ft. Washington STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: BUD
ATTORREY AGGENT INFORMATION:
NAME: GOODMAN, ROSANNE
REGISTRATION NUMBER: 52,534
REFERENCE/DOCKET UNBER: A0856
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 962-4130
TELEFONE: NOCE TO N
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261
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TITLE: IS REVEALED
TITLE: OF CHROMOSOJ
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6041..625, 60802..6934, 7759..7856, 9444..9573..
1087..11081..12481..12613, 13702..13799,
14977..15115, 15534..15757, 16950..17082,
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AUTHORS: Kuang, W-J
AUTHORS: Dennison, O E
AUTHORS: Beatie, W G
AUTHORS: Dentison, J W
AUTHORS: Dentison, J W
AUTHORS: Dugaitzyk, A
IIILE: MOLECULAR STRUCTURE OF THE HUMAN ALBUMIN
"TILE: GENE IS REVEALED BY NUCLEOTIDE SEQUENCE WITH
"TLE: CENE OF CHROWOSOME 4
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                                                                                                     NAME/KET: exon
LOCATION: 15534..15757
OTHER INFORMATION: /number= 12
                                                                                                                                                                                                                       NAME/KEY: intron
LOCATION: 15758..16949
OTHER INFORMATION: /number= 12
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LOCATION: 17083..17696
OTHER INFORMATION: /number= 13
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LOCATION: 17697..17764
OTHER INFORMATION: /number=14
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OTHER INFORMATION: /number= 14
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OTHER INFORMATION: /number= 15
                                                  OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /prod
ATURE:
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PUBLICATION INFORMATION:
AUTHORS: Minghetti, P P
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NAME/KEY: 3'UTR
"TATION: 17742..18697
                          15116..15533
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18535..18697
NAME/KEY: intron
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DATE: 1986
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NAME/KEY: 5'UTR
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                          LOCATION
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Gaps ä Query Match 6.7%; Score 87.2; DB 5; Length 19557; Best Local Similarity 84.6%; Pred. No. 2.2e-17; Matches 110; Conservative 0; Mismatches 18; Indels 2; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 19002 PCT-US92-06300-1

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GENERAL INFORMATION:
APPLICANT: Strebhardt, Klaus; Rubsamen-Waigmann, Helga.
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: TATYCOM
STATE: New York
COUNTRY: U.S.A.
ZUP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: Storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATONREY/AGENT INFORMATION:
NAME: KURT G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/POCKET NUMBER: BAYE 9516-KGB
                                                                                                                                                                                                                                                                                        RESULT 8
US-09-198-122-7/c
: Sequence 7, Application US/09198122
: Patent No. 6180380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGIH: 2503 base pairs
                                                                                                                                                                                                      19736 gggattacaagcac 19749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                             1060 gggattacaggctc 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CI
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
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Fatent No. 6207876
Fatent No. 6207876
GENERAL INFORMATION:
APPLICANT: RELEWS, RODNEY E.
APPLICANT: BATTA, SURJIT X.
APPLICANT: BATTA, SURJIT X.
TITLE OF INVENTION: ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICE AND TITLE OF INVENTION: ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICE AND TITLE OF INVENTION: METHODS FOR THE USE THEREOF
FILL REFERENCE: 1959-04-28
CURRENT APPLICATION NUMBER: 60/083,408
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: 60/083,370
EARLIER PILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTING NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.8%; Score 88; DB 4; Length 35741; Best Local Similarity 83.6%; Pred. No. 1.8e-17; Matches 112; Conservative 0; Mismatches 20; Indels
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
FILING DATE:
                                                                                                                                                               CLASSIFICATION: 436
ATORNET/AGENT INFORMATION:
NAME: Wondow, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8121-13 US2
TELEPOMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHRANCIERISTICS:
LENGTH: 817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-832-877-56
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens US-09-301-665-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1062 gattacagge 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 GATTATAGGC 329
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LENGTH: 36741
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Gaps 5; Ouery Match 6.7%; Score 87.6; DB 4; Length 2503; Best Local Similarity 84.1%; Pred. No. 4.8e-18; Matches 111; Conservative 0; Mismatches 19; Indels 2

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1061 ggattacaggetet 1074
                   RESULT 3
US-08-724-394A-21/C
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                                                                                                                                                                                                                                                  APPLICANT: Feder, John N.
APPLICANT: Eder, John N.
APPLICANT: Lauder, Peter M.
APPLICANT: Lauder, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Truchihashi, Zenta
APPLICANT: Truchihashi, Zenta
APPLICANT: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITT: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 89.6; DB 2; Length 246240;
84.3%; Pred. No. 1.7e-17;
Live 0; Mismatches 19; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: DATUM DATE: PATENTIN BC-DOS/MS-DOS
SOFTWARE: PATENTIN BC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                     Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELERAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Loral Similarity 84.39
Matches 113; Conservative
                                                                          1066 acaggete 1073
                                                                                                              161 ACAGGCGC 154
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                                                                                                                                                                   RESULT 2
US-08-724-394A-20/c
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US-UB-1/44-394A-11/C

Sequence 21. Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Lauer, Peter M.

APPLICANT: Huddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Wolff, Roger K.

CORRESPONDENCE ADDRESS: 31

CORRESPONDENCE ADDRESS: 31

CORRESPONDENCE ADDRESS:

ADDRESSE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Townsend and Townsend and CREW LLP

STREET: USA

CONDUTER: LOS

COUNTRY: USA

ZIP: 94111-3834

COMPUTER: Elappy disk

COMPUTER: Datenin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 35,136

ATTORNEY ABCLICATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 35,136

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 246240;
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6.9%; Score 89.6; DB 2; Length 2
Best Local Similarity 84.3%; Pred. No. 1.7e-17;
Matches 113; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1061 ggattacaggetet 1074
||| ||||||||||||
8607 GGACTACAGGCGCT 8594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-576-0300
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298 HLIVIQIYGNLFSGIIISGFGRL--------RNLTELYLWRN 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 LFQTREQDDWGFISDLTNCSKLQTLN----LGENNLGGVLPNSFSNLSTSLSFLALELN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 HRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPRTSSKYFNFTTEDHKMVEALRVWAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 VWDGTRTPFPSWRVLIQDLVL----EGDL-SHIHRLQNLTIDILVYDNHVHVARSLKVG 236
                                                                                                                                                    APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
3.0%; Score 99; DB 2; Length 1025;
Best Local Similarity 19.6%; Pred. No. 0.81;
Matches 129; Conservative 84; Mismatches 220; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                            SFLRI-----YSLH--TKLQSMN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
                                                                                                    : Sequence 4, Application US/08567375
: Patent No. 5952485
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
            589 FINCSSLK 596
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                                                                              US-08-567-375-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 -----GAATGWPSMARIAQSTEVLFQGQASLDC---GHGHPDGRRLLLSSSLVEALDVWA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GT------RIPFPSWRVLIQDLVLEGDLSHIH-RLQNLIIDILVYDNHV----HV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 GVFSAAAGEGQERRSPITIALCLER-----MSELQARAKRVSWDFKTAESHCKEGDQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 ARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATILTDHQYLERTPL- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 ------CAILKQKAPQQYRIR-AKLRSYKP-RRLFQSVKLHCPKCHLLQEVPHEGD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 YKLVPDPVKNIYIZLTAGKEVRRIRVANCNKHKSCSECLTAIDPHCGMCHSLQRCTFQGD 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 3.1%; Score 103.5; DB 4; Length 1568; Best Local Similarity 20.3%; Pred. No. 0.58; Matches 99; Conservative 60; Mismatches 162; Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 KETQGIT-----SSGFASLIF-----EGTLGAPIIPRTSSKYFNFTTEDHKMV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 LSNECLLLIEGGTLSEICKLSNKFNSV----IPVRSGHEDLELLDLSAPFLIQGTIHHYG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 CVHSENLENWLDI -- SSGAKKCPKIQI -- -- IRSSKEKITVIHVG -- -- -- SFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LDIIFQDGATKTPVVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILP
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC COMPATIBLE
COMFUTER: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
CORRESPONDENCE ADDRESS:
ADDRESSE: Janis C. Hen
STRET: 51 University St
CITY: Seattle
CITY: WA
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-459-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKOCSSLR 510
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                                 1041 RWDLNKFEFASNIMNSSMKSVGEVMSIGRIFEESIQKSLRCIDDNYLGFSNIYC----- 1094
                                                                                                                                                                  1246 EHDVLPLNMKRK------KICTLNNKRNANKKVHV-KNHLYNEVVDDKDTOLHKEN 1295
                                                                                                                                                                                                                                                                                                                                                                               1296 NNNNN-----HNSGNVENKCKLNKESYGYNNSSNCINTNNINIENNIC----HDISINKN 1346
                                                                                                                                                                                                                                                                                         403
                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 GATKIPVVKLQNISLYDSKIWIIKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGILSEI 463
117 RTSSKYFNFTT----EDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKA 172
                                                                                                                                           231 RSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKK 290
                                                                                                                                                                                                                                                                                                                                                                                                                             CK--LSNKFNSVIPVRSGHEDLELLDL,SAPFLIQGTIHHYGCKQCS-----SLRSIQNL 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 ETYGLSFIDLVRIFKSDKITCIDHVAAI-------FGV:HPIJA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 EVDGASF -- LLKVWDGTRIPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 RSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGG---TSYGRGIRVL---PES--- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      1095 - IDWDE--KKIIEELKNPSPK-RIDAIHQAFHLNMPMDKIHELTHIDYWFL-----
                                                                                                                                                                                                                                                                                 344 ERTPLCALLKOKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING HELICASE ACTIVITY AND METHOD THEREFOR
                                                                    173 EVDGASFLLKVWDGTRTPFPSWRV--LIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVA
                                                                                                                                                                                                           291 DLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATI--LIDHQYL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%; Score 105; DB 4; Length 647; 17.7%; Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPIL ACTURED #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,909
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APPLICATION NUMBER: US 60/083,942
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09300909
Patent No. 6306580
GENERAL INFORMATION:
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Best Local Similarity 17.7%
Matches 88; Conservative
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HOLECULE TYPE: protein
US-09-300-909-17
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TITLE OF INVENTION: HEI
NUMBER OF SEQUENCES: 2'
COMPUTER READABLE FORM:
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NN 1403
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US-09-300-909-17
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---- NSDVDQLKKDLES--ANLTANQH------SDVICQSEP 311
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                                                                                                         304 LEPPKLRSPVAALYWYRTGISNISVVIGDTPEWIQRLTVIQHGIDDSVFDLSDMV-QWAF
                                                                                                                                                                                                               363 DNEYTDESDIAFNYAMLADCHSNAAAFLKSNCQAKYVKDCATM----CKHYK-RAQKRQM
                                                                                                                                                                                                                                                                          370 KPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPVVKLQNTSLYDSKIWTTKNQ
                                                                                                                                                                                                                                                                                                                                                                                   430 KGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVI---PVRSGHEDLELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 DLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTS~~WIPSSVAEALGIVPLQYVFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 TFTLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFCPP-----GIK
                                                                                                                                                                DDSFPSSGSVSL--YEVERCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSY
                                                                                                                                                                                                                                                                                                             484 CMSLMHFLQGTVISY------VNSTSHFWLEPLADAKLAM-----
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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. Dubose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAHURIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seatle
STATE: WA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/181,706
FILLING DATE: October 28, 1998
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09181706
Patent No. 6130068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
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ELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597 IDAYPWLECFIKSYNVTN 614
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                                                    282
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LENGIH: 1144 amino acids
                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                           HOLECULE TYPE: protein PCT-US95-07754A-4
                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      amino acid
3Y: linear
                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                         387
                                                                                                                                                                                                                   ---THM---SPSWILLKL----CDVQPMQ--- 160
                                                                                                                                                                                                                                            -----ALKVWGSLLHNLRLTEWRSAIEHMKNNSYSGIIDKLKISYDGLEPKQQEM 437
                                                                                                                                                                                                                                                                      161 YFDLTCQLLGKAEVDGASFLLKVWD-----GTRTPFPSWRVLIQDLVLEGDLSHIHR 212
                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                 272 GRGIRVLPESNSDVDQLKKDLESANL-TANQHSDV------ICOSEPDDSFPSSGS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                      595 LKMLVHLQLRHNSLRHLWTETKHLPSLRRIDLSWSKRLTRTPDFTGMPNLEYVNLYQCSN 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CQQLSATILTDHQYLERTPLCAILK------QKAPQOY-RIRA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLRSYK------PRRLFOSVKLHCPK------CHL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854
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                                                                                                                                                                                                                                                                                                                                                                                                 SSTLRF---SNQAVKNMKR-LRVFNMGRSSTHYAIDYLPNNLRCFVCTNYPWESFPSTFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTIHHYGCKQC
                                                                                                                                                                            335 LIEKNDIIYEVTALPDHESIQLFKQHAFGKEVPNENFEKLSLEVVNYAKGLPL-----
                                                                                                                                                                                                                                                                                                FLDIACFLRGEEK----DYILOILESCHIGAEYGLR------ILIDKSLVFISE
                                                                                                                                                                                                                                                                                                                           LONLTIDILLY DNHVHVARSLK-VGSFLRIYSLHTKLOSMNSENOTMLSLEFHLHGGTSY
                                                                                                                                                                                                                                                                                                                                                      482 YNQVQMHDLIQDMGKYIVNFQKDPGERSRLW-LAKEVEEVMSNNTGTMAME--AIWVSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQEVPHE-GDLDI IFQDGATKTPVVKLQNTSLYDSK IWTTKNQKGRKVAVHFVKNNGILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 SSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFTLDDGTGVLEAY-LMDSDKF
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GENERAL INFORMATION:
APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
NUMBER OF SEQUENCES: 6
                                                                                                     3.7%; Score 122; DB 5; Length 1144; Similarity .18.2%; Pred. No. 0.0039; Conservative 106; Mismatches 200; Indels 39
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LDDAHNDTMYNLFAYTMFQNI 953
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           : 1144 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                 FTTEDHKMVEALRVWAS ----
SEQUENCE CHARACTERISTICS
                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                    HOLECULE TYPI
PCT-US95-07754A-2
                                                                                                                                Matches 135;
           LENGTH:
                                                                                                        Query Match
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Best Local Similarity 18.2%; Pred. No. 0.0039;
Matches 135; Conservative 106; Mismatches 200; Indels 300;
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILIATION NUMBER: PCT/US95/07754A
FILING DATE:
ADDRESSEE: Margaret A. Connor, USDA-ARS-STREET: 800 Buchanan Street
CITY: Albany
STATE: CA
COUNTRY: USA
21P: 94710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0094.94
                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-577
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                Indels 300;
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Patent No. 557106
PAPELICANT: Baker, Barbara J
APPLICANT: Miltham, Steven A
TITLE OF INVERTION:
PLANCES: 6
NUMBER OF SEQUENCES: 6
                                                                                                      Length 1143;
                                                                                                Ouery Match 3.7%; Score 122; DB 5; L
Eest Local Similarity 18.2%; Pred. No. 0.0039;
Matches 135; Conservative 106; Mismatches 200;
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LENGTH: 1143 amino acids
TYPE: amino acid
TOPOLOGY: linear
               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 : LENGTH: 1143
: TYPE: anino
: TOPOLOGY: 11
: MOLECULE TYPE:
PCT-US95-04589-108
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US-08-261-663A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.7%; Score 122; DB 1; Length 1144; Best Local Similarity 18.2%; Pred. No. 0.0039; Matches 135; Conservative 106; Mismatches 200; Indels 300;
                                                                                                                                                   ZIP: 94710
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                         Connor, USDA-ARS
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/261,663A
             ADDRESSEE: Margaret A. Conno
STREET: 800 Buchanan Street
CITY: Albany
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 30043
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-663A-2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
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COUNTY CO	FILI	; TELECO; ; TELE; ; INFORMATI; ; SEQUENATI; ; TYPE; ; TYPE; ; TOPOI ; MOLECUI	Ouery Matc Best Local Matches 1	335 125 388 161 161 438 438	Db 482 YNQ Oy 272 GRG Db 539 SST Oy 321 Db 595 LKM OY 329 Db 655 LEE OY 365 KLR6 OY 365 KLR6 OY 365 KLR6 OY 361 LOEV OY 447 LSNE
Db 335 LIEKNDIIYEVTALPDHESIQLEKQHAFGKEVPNENFEKLSLEVVNYAKGLPI 387 Oy 125 FTTEDHKAVEALRVWAS	OY 213 LONITIDILYTDNHYVHVARSLK-VGSFLRIYSLHTKLOSMNSENOTMLSLEFHLHGGISY 271 1	595 329 655 365 714	300 LOEVER-GDLDIIEQDGAIKTPVVKLONTSLYDSKIWTTKNOKGRKVAVHFVKNNGILP 773 LESLPEEIGDLDNLRVFDASDTLILRPPSSIIRLNKL-IILMFRGFKDGVHF 447 LSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIGGIIHHYGGKQC 824	Oy 507 SSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFWHTFTLDDGTGVLEAY-LMDSDKF 565 1 1:: : : : : :	Sequence 108, Application US/08310912A Sequence 108, Application US/08310912A Sequence 108, Application US/08310912A Sequence 108, Application US/08310912A GENERAL INFORMATION: APPLICANT: Staskawicz, Brian J. APPLICANT: Staskawicz, Brian J. APPLICANT: Breat, Andrew F. APPLICANT: Mandel Service F. APPLICANT: Mandel Service F. APPLICANT: Mindrinos, Michael N. APPLICANT: Windel Barbara N. APPLICANT: Windel Service Service FAMILY, PRIMERS, PROBES, AND DETECTION TITLE OF INVENTION: METHODS TITLE OF INVENTION: METHODS CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA

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Gaps
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MLVHLQLRHNSLRHLWTETKHLPSLRRIDLSWSKRLTRTPDFTGMPNLEYVNLYQCSN 654
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773 LESLPEEIGDLDNLRVFDASDTLILRPPSSIIRLNKL-IILMFRGFKDGVHF------ 823
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WEDIUM TYPE: FLOPPY disk

WEDIUM TYPE: FLOPPY disk

WEDIUM TYPE: FLOPPY disk

COMPUTER: Bub PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B

APPLICATION NUMBER: US/08/310, 912A

CLASSIFICATION NUMBER: US/08/310, 912A

CLASSIFICATION NUMBER: US/08/210, 94

TORNEY/AGENT INFORMATION: 536

TORNEY/AGENT INFORMATION: By AME: Lech, Karen F.

REGISTRATION NUMBER: 35, 238

REFERENCE/DOCKET NUMBER: 00786/254001

TELEPHONE: (617) 542-5970

TELEFAX: (617) 542-5970

TELEFAX: (617) 542-5906

RAMATION FOR SEQ ID NO: 108:

CLENGTH: 113 amino acids

TYPE: Amino acids
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                                 1096 OWSEAMAKGAIPYLYGVYTAIVMKECKNLLT---LNTLVAAHGGVVMDTFPGKELFNVGS 1152
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MEDIARE-94150718; PubMed-7906398;
Wilson R., Annscough R., Anderson K., Baynes C., Berks M.,
Bonfleld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Crazton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Rershaw J., Rirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callagian M.,
Barsons J., Percy C., Rifken L., Staden R., Sunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas R., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 TMLSLEFHLH-GGTSYGRGIRVLPE--SNSDVDQLKKDLESA-----NLTANQHSDV 305
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          ------OGTIHH-YG-----CKOCSSLRSIONLNSLVDKTSWI-----PSSVAEALGI 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 RYFDVLAQVHSVVETINGAQMLRVWRGRKFGPGASAERRERRLFHVTQDSFKRYIVPPNP 84
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                                                                                                                                                                                                                                                                                                         Baynes C.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
EMBL: 283110; CAB05525.1; -.
SEQUENCE 251 AA: 28987 MW; 8F2F231D01C38B9F CRC64;
                                                                                                                                                                               Last sequence update)
Last annotation update)
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09Y4E4;
01-NOV-1999 (TrEMBLrel: 12,
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01.JUN-1998 (TrEMBLrel.
01.JAN-1999 (TrEMBLrel.
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"Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).

REMBL; AB011152; BAA25506.1; -...

Interpro: IPR001048; RhoGAP.

RICHEPTO: IPR001049; PH.

R pfam; PF00169; PH; 4.

R Pfam; PF00169; PH; 4.

R Pfam; PF00412; ArfGap: 1.

R PRINTS; RR00405; REVINTRACTNG.

R PROSITE; PS50003; PH DOMAIN; 3.
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Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 FE----IYLPSERVFLFGAETS---QAORKWTEAIAKHFVPLFA-ENLTEAD----Y
                                                                                                                                                                                                                                                               Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 116; DB 4; Length 1044;
22.0%; Pred. No. 1.2;
iive 83; Mismatches 212; Indels 148;
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68E22A66DEAA53BD CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA0580 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 ILVYDNH-VHVARSLKVGSFLRIYSLHTKL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1044 AA; 119463 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00233; PH; 3.
SMART; SM00324; RhoGAP; 1.
SEQUENCE 1044 AA; 11946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00105; ArfGap; 1.
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Best Local Similarity 22.0'
Matches 125; Conservative
                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356
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                                                                                               536
                                                                                                                                                -----NCGVLKQYRDI-KVIKKGSYCEISQNSVIIDIS 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IQVYKKETQGITSSG------FASLIFEGTLGAPIIPRISSKY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GDLSHIHRLQNLTIDI-LVYDNHVH--VARSLKVGSFLRIYSLH 245
311 LLPHIMGYTADSPPPAGLINPLE------ENVPHKFDSFQVTLVNANHCPGAVMFVF 361
                                                          417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDV-----QPMQYFDLTCQLLGKAEV- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTANQHSDV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 VTIVDQTNVKLTCL------85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATNYIYTP-----LNQ----LKGGTIV----NVYGVVKFFKPPYLSKGTDYCSV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 QDPADWDSRLTNKKGTEEIIKKANQIWIDNNWQIFHEYVLLYNELDVWLLLEVFEAFRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNF-----LPESLASLANKLTTLKYTPDKFKDAFNSGKGEFPYEWFD-DFNKLEEIEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|:: | | DHHILLEQLLNRDSKHNTCRGKSINKMDVITHKDILSDFIRITFKDT------
                                                                                                                             -----ELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIP-SSVAEALGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DGASFLLK----VW-DGTRTPFPSWRVLIQD----LVLE-----
                                 362 EGSKIEEIAGGAVLCTGDFRADKMFLESLKPGNOLHWMTE----IKFGIIYLDNTYFSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANLIDEAGERFRCLACNKNKKGKYYYARHYGLGIFGYYCRSCFLAHNNTFIVYFHNFKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
3.7%; Score 123; DB 12; Length 1115;
Best Local Similarity 18.9%; Pred. No. 0.35;
Matches 143; Conservative 121; Mismatches 250; Indels 244;
                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
STRAIN-TAMANASHI ISOLATE;
MARAGAKI M. NONASE K., Bando H.:
"orfl, orf2, orf3, orf4 (DNA segment VD1) [parvo-like virus, isolate, host-silkworm, Genomic, 6542 nt].";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033596; BAA65362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7C0DA2DCFA746428 CRC64;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                   Parvo-like virus.
Viruses; ssDNA viruses; Parvoviridae;
NCBI_TaxID=45454;
                                                                              445 LPLSNEC----LLLIEGGTLSEICKLSNKFNSVIPV-RSGHEDL-
                                                                                                                                                                           537 PLQIVEVMIFILDDGIGVLEAYLMDSDKFFQIPASE 572
                                                                                                                                                                                          516 MLYYTF------GNGV-----NDDEGIIRIPYSD 538
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                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nonstructural protein.
SEGGENCE 1115 AA; 128304 MW;
                                                                                                                                             : | | | | : | 471 ERKVISDLLDFSS-----
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                           01-JUN-2000 (TrEMBLIE) NONSTRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                   01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                              090MH2
                                                                                                                                                                                                                                      RESULT 11
Q9QMH2
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MEDLINE=95007759; PubMed=7923359;

Miltham S., Dinesh-Kumar S., Choi D., Hehl R., Corr C., Baker B.;

Whitham S., Dinesh-Kumar S., Choi D., Hehl R., Corr C., Baker B.;

The product of the tobacco mosaic virus resistance gene N: similarity

to toll and the interleukin-1 receptor.";

Coll 78:100-1115(1994).

EMBL: U15605; AAA50763.1; -.

Mendel: 13926; Nicqui: 4265;13926.

InterPro; IPR000157; TIR.

InterPro; IPR000157; TIR.
693 TKYANIEDVDETIVYLD--VNTMYSYCMKQKLANKYLGTLDTLPDNYDS------DDN 742
                                                      ICQ-SEPDDSFPSSGSVSLYEVERCQQLSATI----LIDHQYLERTPLCAILKQKAPQQYR 361
                                                                                                                                                                        421
                                                                                                                                                                                                                           833
                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                    541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 FVMTFTLDDGTGVLEAYLMDSDK----- FFQIPASEVLMDDDLQKSVDMIMD---- 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 YELFDVIPEGSTATMLY-TDTDSVIFKFKGFNGVHPYKYLLTTSLASKLDIPINKDGSFG 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 IIYKNGDIVRFHRL----KIQVYKKETQG--ITSSGFASLTFEGTLGAPIIPRTSSKYFN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Hagnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                             743 FCYFIKGDFSYP-----EYLHDLPAHLSMPLMPHQY--NNKLCTTFLDK--KDML
                                                                                                                                                                                                      422 KIWTTKNOKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHE
                                                                                                                                                                                                                                                                                                                                        -----TDPGTK-DYYKLKNNALF------GKTCENVFKY--KIFSVTNVNSGDR
                                                                                                                                                                                                                                                                                                                                                                                                 482 DLELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                        874 ENKCMSKAKSHITLGNCILY--EECVT-----RYLLDKPIQIGFTILELAKLMIYEFI
                                                                                                                                                                     362 IRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPVVKLQNTSLYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1EC5B36D4C4BCBB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIRUS RESISTANCE (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 3.7%; Score 122; DB 10; Best Local Similarity 18.2%; Pred. No. 0.44; Matches 135; Conservative 106; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 -MFCPPGIKID--AYPWLECFI----KSYNVTNGTD 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1144 AA; 131485 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001611; LRR.
InterPro: IPR001861; LRR.
InterPro: IPR003591; LRR_typ.
InterPro: IPR003592; LRR_out.
Pfam; PP00560; LRR; 5.
Pfam; PP005931; NB-ARC; 1.
Pfam; PP01881; 1.
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SMART; SM00370; LRR; 1
SMART; SM00369; LRR_TYP; 1.
SMART; SM00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Q40392
                                                         306
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23;

Gaps

261 273 324 364

SEQUENCE FROM N.A.

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81 FHRLKIQVYKKETQGI----TSSGFASLIFEGTLGAPIIPRISSKYFNFTTEDHKMVEAL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 VNVYGVVKFFKPPYLSKGTDYCSVVTIVD--QTNVKLTCLLFSGNYEALPIIYKNGDIVR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VNLIGVIVELG --- FSNGSDCSCTLKIVDPWYSGSGLPVKFVARTIRDLPRVESIGDIIL 81
                                                                                                                                                                                                                                                                                                         QLLGKAEVDGASFLLKVWDGTR-----TPFFPS---WRVLIQDLVLEGDLSHIHRLQNL 216
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                  120 -----SKYFNFTTEDHKMVEALRVWAS----THMS-PSWTLLKLCDVQPMQYFDLTC 166
                                                                                                                                                                                                                                              158 EEQFALLLNKIWDEGTNKHKNGELLSTSSARQNQTGLSYPSVSFSLLSQITPHORCSFYA 217
                                                                                                                             72 IYKNGDIVRFHRLKIQVYKKETQGITSSGFA-----SLTFEGTLGAPIIPRTS---- 119
                                                                                                                                                           Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen
                                     KGGTIVNVYGVVKFFKPPYLS-KGT-DYCSVVTIVDQT----NVKLTCLLFSGNYEALPI 71
                                                                         218 QVI-KTWYSDKNFTLYVTDYTENELFFPMSPYTSSSRWR------GPFG-----RF
                                                                                                                                                                                                                                                                                                                                                                                                 217 TIDILUYDNHVHVARS-LKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTS--YGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 GIRVLPESNSDVDQLK--KDLESANLTANQHSDVICQS------EPDDSFPSSGSVSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 SIEKVDSEEPELNEIKSRKRLYVQN------CONGIEAVIEKLSQSQOSENPFIAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 463;
83; Mismatches 177; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 VKLHCPKCH-----LLQEVPHEGDLDIIF--QDGATKTPVVKLQNTSLYD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB006700; BAB08953.1; -. SEQUENCE 463 Aa; 53630 MW; A735DBF109155D7D CRC64;
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Last annotation update)
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8-st Local Similarity 22.8%; Pred. No. 0.00029;
Matches 94; Conservative 59; Mismatches 164
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MEDLINE=98069011; PubMed=9405937;
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(TrEMBLrel. 16, I
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DNA Res. 4:291-300(1997).
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       109; Conservative
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GB|AAD29059.1.
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RA Arawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
R Filstohmann W., Gaasterland T., Gissi C., King B., Rochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Watchlonni L., Mashima J., Mazzarelli J., Hombaerts P.,
RA Gasaki H., Sato R., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wymshaw Booris A., Yoshida K., Hasegawa Y., Rawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; *Punction of a full-length mouse cDNA collection.";
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EMBL, 299126; CAB16192.2; -.
Hypothetical protein.
SEQUENCE 555 AA: 64111 MW; A79DAA95A0C4F803 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watch 9.7%; Score 324; DB 11; Length 1 Local Similarity 73.3%; Pred. No. 3e-19; les 63; Conservative 6; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AA; 12740 MW; 08BBB9FC5D0C7088 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 64.1 KDA PROTEIN C26H5.06 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 199.5; DB 3;
Pred. No. 6e-08;
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                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE=EMBRYO; ... WEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK013364; BAB28810.1; ..
MGD; MGI:1920086; 2810458H16Rlk.
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NCBI_TaxID=4896;
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SEQUENCE

Query Match

Matches

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17;

Gaps

STRAIN-972;

Query Match

SPAC26H5.06

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 HLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 GNMKKKVKLS----KEHOSLEENQRQTRSKRKATSD------TLESPPKIIP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCHLLQEVPH----EGDLDIIFQDGATKTPVVKLQNTSLYDSKIWTTKNQKGRKVAVHFV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CDVQPMQYFDLTC---QLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDL----VLEG 205
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ACT_SITE 90 90 BY SIMILARITY.

ACT_SITE 584 584 BY SIMILARITY.

ACT_SITE 593 593 BY SIMILARITY.

SEQUENCE 785 AA; 88207 MW; 50AA2817A60810AF CRC64;
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               MEDLINE-99026138; PubMed-9806842;
Fjiwara T., Saito A., Suzuki M., Shinomiya H., Suzuki T.,
Takahashi E., Tanigami A., Ichiyama A., Chung C.H., Nakamura Y.,
                                                                                                   "Identification and chromosomal assignment of USP1, a novel gene encoding a human ubiquitin-specific protease.";
Genomics 54:155-158(1998).
                                                                                                                                                                                                                                                Wiemann S., Well B., Wellenreuther R., Gassenbuber J., Glassl S., Ansorge W., Boecher H., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Rochrer K., Strack N., Mewes H.-W., Ottenwelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Rlein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."

"Genome Res. 11:422-435(2001).

"I. CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                UBIQUITIN + A THIOL.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWK AS
FAMILY 2 OF UBIQUITIN CARBOXXL-TERMINAL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 104; DB 1; Length 785: 19.8%; Pred. No. 5.9;
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                                                                                                                                                                                                               TISSUE-Testis;
MEDLINE-21154917; PubMed-11230166;
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Pfam: PF00443; UCH-2; 1.
PROSITE; PS00972; UCH_2_1; 1.
PROSITE; PS00973; UCH_2_2; 1.
PROSITE; PS0035; UCH_2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001394; UCH-2.
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                 Fanaka K.;
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STRAIN-MOPN / Nigg:

XX MEDLINE-20150255; PubMed=10684935;
XX MEDLINE-20150255; PubMed=10684935;
XX MEDLINE-20150255; PubMed=10684935;
XX Read T.D. HCKey E.K. Shen C., Gill S.R., Heidelberg J.F.,
XX Mite O., HCKey E.K., Shenc C., Gill S.R., Heidelberg J.F.,
XX Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
XX Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
XX Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
XX Esone sequences of Chlamydia trachomatis MoPn and Chlamydia

The neumoniae AR39 ":

Nucleic Acids Res. 28:1397-1406(2000).

STRANDED ON NU-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

STRANDED ON UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

STRANSPORTERS). CONTAINS FOUR ABC DOMAINS.
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                                             KNNGILP------LSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHEDL--ELL 486
                                                                        487 DLSAPFLIQG-TIHHYGCKQCSSL----RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYV 541
                                                                                                                                                                              EK ---- LFQGQLVLRTRCLECESLTERREDFQDISVPVQEDEL -- SKVEESSEISPEPKT 480
                                                                                                                                                                                                                            542 FVMTFTLDDGTGVLEAYLMDSDKFF-----OIPASEVLMDDDLQKSVDMIMDMFCPPGI 595
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320 KYISENESPRPSQKKSRVKINWLKSATKQPSILSKFCSL--GKITTNQGVKGQS----- 371
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Pfam: PF00005; ABC_tran; 2.
PROSITE: PS00211 ABC_TRANSPORTER; 1.
SOS response; Excision nuclease; DNA-binding; Repeat; DNA-binding; Zinc finger; Complete proteome.
NP_BIND 625 632 ATP (POTENTIAL).
NP_BIND 649 971 ATP (POTENTIAL).
NP_BIND 964 971 ATP (POTENTIAL).
NP_BIND 1509 1516 ATP (POTENTIAL).
NP_BIND 742 C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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20-AUG-2001 (Rel. 40, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia muridarum.
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                                                                                                                                                                                                                                                                                                                        595 KIDAY 600
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09PK60;
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQKQALEE-----LKQSVQQLRCTEAKFSAQK-------ELLEQKVQE--- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 -KDKQQVKKS---YIGVHQQIEAEMIKVTKTELEKLKCSYRQLIKEMNSAKEKYK--EAL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 RVWAST------HMSPSWTLLKL--CDVQPMQYFDLTCQLLGKAEVDGASFL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AKGKETEKAKERYDKATMKLHMLHNQYVLALKGAQLHQNQYYDITLPLLLDSLQKMQEEM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDIL----VYDNHVHVARSLKVG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 SFLRIYSLHTKLQ-----SMNSENQTMLSLEFHLHGGTSYGRGI------RV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 LPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATIL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIIFQDGATKIPVVKLQNTSLYDSKIWTIKNQKGRKVAVHFVKNN--GIL--PLSNECLL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

V -> L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KYFNFITEDHKMVEAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 TDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 LSKGTDYCSVVTIVDQTNVKLTCLLFSGNYEALPIIYK-----NGDIVRFHRLKIQVY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proto-oncogene; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Mismatches 213; Indels 214;
                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Tyrosine-protein kinase; Proto-oncogene; AIP-b
Phosphorylation; Nuclear protein; SH2 domain; Polymorphism.
DOMAIN 460 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 107; DB 1; Length 822; 20.0%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId=VAR_006282.
0491CD69392DB415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 KKETQGITSSGFASLIFEGTLGAPIIPRISS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                                Pfam: PF00061; FCH: 1.
Pfam: PF00069; pkinase: 1.
Pfam: PF00017; SH2: 1.
PRINTS: PR00109; TYRKINASE.
SWART: SW00055; FCH: 1.
SWART: SW00055; FCH: 1.
SWART: SW00199; TYRK: 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP: 1.
PROSITE; PS500109; PROTEIN_KINASE_TYR: 1.
PROSITE; PS50011: PROTEIN_KINASE_TYR: 1.
PROSITE; PS50011: PROTEIN_KINASE_TYR: 1.
                                                                                                                                                                                 Interpro; IPR000719; Euk_pkinase.
Interpro; IPR001060; FCH.
Interpro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                     InterPro; IPR001245; Tyr_kin.
                                                                                                                      EMBL; J03358; AAA61190.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 20.0 Matches 127; Conservative
                                                                                                                                    PIR; A31943; TVHUFE.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                    MIM; 176942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
MOD_RES
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96249699; PubMed-8830262;
Barak I., Behari J., Olmedo G., Guzman P., Brown D.P., Castro E.,
Barak I., Behari J., Olmedo G., Guzman P.,
Barak I., Behari J., Olmedo G., Guzman P.,
Malker D., Westpheling J., Youngman P.;
Tructure and function of the Bacillus SpoilE protein and its
localization to sites of sporulation septum assembly.";
HOI. Microbiol. 19:1047-1060(1996).
C. !- FUNCTION: NORMALLY NEEDED FOR PRO-SIGMA E PROCESSING DURING
SPORULATION BUT CAN BE BYPASSED IN VECETATIVE CELLS. ACTIVATES
SPORULATION BUT CAN BE BYPASSED IN VECETATIVE CELLS.
C. CATALYTIC ACTIVITY: A PHOSPHORPOTEIN + H(2)O. A PROTEIN +
C. I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. POLAR SEPTUM (BY
SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
 437
                                     494
                                                                      438 AVGSSALSDMISISEKPLAEQDWYHGAIP---RIEAQELLKKQGDFLVRESHGKPGEYVL 494
                                                                                                            -----IHHYGCKQCSSLRS-IQNLNSLVDKT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 202; Indels 208; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVI--IVDQTNV----KLTCLLFSGNYEALPIIYKNGDIVRFH------RLKIQVYKKET 93
----NDGKEPPPVVNYEE----DARSVTSMERKERLSKFESIRHSIAGIIRSPKS----
                                                                                                                                               495 SVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTKQVITKKSGVVLLNPIPKDK
                                       454 LIEGGILSEICKLSNK-----FNSVIPVRSGHEDLELLDLSAPFLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.2%; Score 105; DB 1; Length 585; 19.4%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
STAGE II SPORULATION PROTEIN E (EC 3.1.3.16) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PP2C-LIKE.
90E9ACF1D3E21D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                   523 SWIPSS----VAEALGIVPLQYVFVMTFTLDDGTGV 554
                                                                                                                                                                                                            555 KWILSHEDVILGELLG--KGNFGEVYKGTLKDKTSV 588
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                                                                                                                                                                                                                                                                                                                    585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sporulation; Hydrolase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U26836; AAB58072.1; -.
InterPro; IPR003589; PP2C_catalytic.
InterPro; IPR003588; PP2C_sig.
SMART; SM00332; PP2Cc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
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                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baci/llus megaterium.
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585 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1404;
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Best Local Simi
Matches 120;
                                                                                                                                                                                                                                                                                                                    SP2E_BACME
P49600;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
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WEDLINE-92218864; Pubbed-1313846;

A MEDLINE-92218864; Pubbed-1313846;

A MEDLINE-92218864; Pubbed-1313846;

A Mang P.L., O'Farrell S., Clayberger C., Krensky A.M.;

"Identification and molecular clouling of tactile. A novel human T

cell activation antigen that is a member of the 1g gene

superfamily ";

"I Immunol 148.2600-2608(1992).

"I IMMUNOLUBING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVALLY

ENOATHOLUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVALLY

ENOATHOLUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVALLY

"I ISSUE SPECIFICITY: EXPRESSED ON NORMAL I CELL LINES AND CLONES,

AND SOME TRANSFORMED T CELLS, BUT NOW OTHER CULTURED CELL LINES

"I ISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS ON ACTIVATED B CELLS.

"I ISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS ON PERIPHERAL T CELLS

"I STRONGLY UP-REGULATED AFTER ACTIVATION, PEAKING 5 TO 9 DAYS

AND IS STRONGLY UP-REGULATED AFTER ACTIVATION, PEAKING 5 TO 9 DAYS

AND IS STRONGLY UP-REGULATED AFTER ACTIVATION, PEAKING.

"I SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

"I SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOWAIN."

"I STRUBE-PROW, NOTE-CD guide CD96 chur".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                  445
                                                                                                                                                                                                                                                                                                   666 FPDGFELKVECITLQRRLDINLIFINWINDVSSRNLNFDFDSKIFYLTQSESAE-----S 720
                                                                                                                                                                                                                                                                                                                                                                    550
                                                                                                                                                                                                                                                                                                                                                                                              121 PLRLSVSIDFDPCSFCKEIRTLAHLGYN-----IPSQLMELASC--LQRIQLIAMCLID 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 GIGVLEAYLMDSDRFFQIPASE----VLMDDDLQRSVDMIMDMF------CPPG 594
                                             ----- OMFITLMRFQ 579
                                                                                         400
                                                                                                                                                                                                                                                                           -----PLSNECLL------LIEGGTLSEIC--KLSNKFNSVIPVRSGHEDLELLDLSA 490
SNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSAILLTDH 340
                                                                                                                                    PLFFRT-----LVNRIKOE--LDLL 609
                                                                                                                                                                                                            PFLIQGT1HHYGCKQCSSLRSIQNLNSLVDKTSW1PSSVAEALG1VPLQYVFVM1FTLDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fomo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
WCBI_TaxID=9606;
                                                                                                                                                                                  ---FQDGATKTPVV---KLQNTSLYDSK-IWTTKNQKGRKVAVH-FVKNNGIL-----
                                                                                         QYLERTPLCAILKQKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 IKI-----DAYPWLECFIKSY-----NVTNGTDNQICYQIFDTTVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAIGRRNFLKNIHPHVENYAYQFSSLTSLLMNKRNAISHTYMQIQEQLFQLDICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
7-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569
                                        551 EDEVIAQLKSLLQYSKTSS-----
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SEQUENCE FROM N.A.
MEDLINE*92218864; F
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ID TACT_HUMAN
AC P40200;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LICQL-LGKAEVDGASFLLKVWDGTRTPFPSWRVLIQ----DLVLEGD----LSHIHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| ::| ::| | ::| | ::
228 KFSCHIRVGPNKILRSSTIVKVFAKPEIP-----VIVENNSTDVLVERRFICLLKNVFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 QLKGGTIVNVYGVVKFFKPPYLSKGTDYC-----SVVTIVD--QTNVKLTCLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KY----FNFTTEDHKMVEALRVWASTHMSPSWTLLK-----LCDVQPMQYFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPRTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 ONLT--ID-ILVYDNH--VHVARSLKVG--SFLRIYSLHTKLQS---MNSENQTMLSLEF
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 569;
                                                                                                              SURFACE PROTEIN TACTILE.
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                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                        IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE V-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PRO/SER/THR-RICH.
PRO-RICH.
                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 110.5; DB 1;
21.8%; Pred. No. 1.2;
ative 72; Mismatches 139;
                                                                                                                                                                                                                                    N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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or send an email to license@isb-sib.ch)
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART: SM00409; IG; 1.
Immunoglobulin domain; Glyco.
                    EMBL; M88282; AAA36662.1;
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569 AA;
                                          PIR; A46462; A46462
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Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                               Viruses: dSDNA viruses, no RNA stage; Tailed phages; Myoviridae;
T4-like phages.
NCBI_TaxID=10665;
                                                                                                                                                                                                                                                         MEDLINE-85257446; PubMed-4018026;
Gram H., Rueger W.;
"Genes 55, alpha gt., 47 and 46 of bacterlophage I4: the genomic
organization as deduced by sequence analysis.";
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Submitted (APR-1987) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: EXONUCLEASE INVOLVED IN PHAGE DNA RECOMBINATION,
REPLICATION, AND REPAIR.
-!- SUBBUIT: CONSISTS OF TWO SUBUNITS: GP47 AND GP46.
-!- SIMILARITY: STRONG TO T5 PROTEIN D13 AND TO YEAST RAD52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; Score 122; DB 1; Length 560; 18.7%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                           3.
                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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D107829431BAB2FC CRC64;
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                                                                                                                           13-AUG-1987 (Rel. 05, Created)
10-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EXENICLEASE SUBUNIT 2 (EC 3.1.11.-) (PROTEIN GP46).
                                                                                                                                                                                                                                                                                                                                        Kutter E., Arisaka F., Kunisawa T., Tsugita A.,
Mesyanzhinov V., Ruger W., Stidham T., Thomas E.
"Bacteriophage T4 genome analysis.";
                                                                                                       560 AA
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                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 478-560 FROM N.A.
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                      341 QY 342
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   "Gatlp, a GATA family protein whose production is sensitive to nitrogen catabolite repression, participates in transcriptional activation of nitrogen-catabolic genes in Saccharomyces cerevisiae.";
   Mol. Cell. Biol. 16:847-858(1996).
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-!- FUNCTION: POSITIVE REGULATOR OF MULTIPLE NITROGEN CATABOLIC GENES.
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Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MEDLINE-95400292; PubMed-7670463;
Murakami Y., Naltou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
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-!- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
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01-NOV-1995 (Rel. 32, Last sequence update)
02-NG-2001 (Rel. 40, Last annotation update)
TRANSCRIPTIONAL REGULATORY PROTEIN GATI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             betwhen the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                               201
                                        114 IIPRT----SSKYF-----NFTTEDH--KMVEALRVWASTHMSPSWIL--LKLC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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VNVVFFSQNFEDLPIIQRVGDIVRVHRARLQHYNDAKQLNVNMYYRSSWCLFIGNDKEAP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Ciliophora; hypotrichs; Euplotida; Euplotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 IP-----RISSKYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVCPMQYFD
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                                                                    129 LEPRVENEDGINNYFSYIPYNFSGKSFIQEGHETKILKDLKKWSKDYFSNNDVVEQVKKA
                                                                                                                               DVQPMQY ----FDLTCQLLGRAEVDGASFLLKVWDGT -----RTPFPSWRVL1QDL
                                                                                                                                                                         DIETAMKNKTDFDLLAKVTEISDNDQYTNTVSLNDSTGQTWTGHLFKRKFPH-----
                                                                                                                                                                                                                                                LVKGDVLRIKSVSAKEDNSLIFSSHSNILK-----FFSFSSIHKKLKSSISSD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 450;
                                                                                                                                                                                                                   VLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQSMNSEN
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InterPro; IPR003415; Telo_bind_alpha.
Pfam; PF02307; Telo_bind_alpha; 1.
DNA-binding; Nuclear protein; Telomere; Multigene family.
SEOUENCE 460 AA; 53360 MW; EDIC141385A0B5FE CRC64;
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21.6%; Pred. No. 0.0001;
ive 74; Mismatches 195;
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01-JUN-1994 (Rel. 29, Last sequence update)
101-JUN-1994 (Rel. 29, Last annotation update)
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Best Local Similarity 21.69
Matches 117; Conservative
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ID TEBH_EUPCR
AC Q06183;
DT 01-JUN-1994 (
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*Crystal structure of the Oxytricha nova telomere end binding protein
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---IIDEMYTPLSQARQEEGDFNVVGKVTQIVHRDYYTSDLRVK 224
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MEDLINE=92035001; PubMed=1840510;
Gray J.T., Celander D.W., Price C.M., Cech T.R.;
"Cloning and expression of genes for the Oxytricha telomere-binding protein: specific subunit interactions in the telomeric complex.";
Cell 67:807-814(1991).
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                                                                                                                                                                                                                                                                                                                  LPESN----SDVDQLKKDLESANLTANQHSD-----VICQSEPDDSFPSSGSVSLYEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 CQQLSATILTDHQYLERTPLCAILKQKAPQQ--YRIRAKLRSYKPRRLFQSVKLHCPKCH
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                                                                                                          DN-----HVHVARSLKVGSFLRIY-SLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 LLQEVPHEGDLDIIFQDGATKT-PVVKLQ-----NTSLYDS--KIWT-TKNQKGRKVAV
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30-MAY-2000 (Rel. 39, Last annotation update)
TELOMERE-BINDING PROTEIN ALPHA SUBUNIT (TELOMERE-BINDING PROTEIN
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NCBL_TaxID=5945;
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MEDLINE-99091054; PubMed-9875850;
Horvath M.P., Schweiker V.L., Bevilacqua J.M., Ruggles J.A.,
Schultz S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92249771; PubMed-1577273;
Mitcham J.L., Lynn A.J., Prescott D.M.;
"Analysis of a scrambled gene: the gene encoding alpha-telomere-binding protein in Oxytricha nova. Genes Dev. 6:788-800(1992).
                                                                                                                                                                                                                                                                                                                                                                                           269 APHSNIMTFVPFSRLAKSLDSQISLSPDKVDKELIKKVILTEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 AA.
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probable membrane protein YFL021w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
C:Date: 0.2-6ep-1995 #sequence_revision 19-Oct-1995 #text_change 06-Feb-1998
C:Date: 0.2-6ep-1995 #sequence_revision 19-Oct-1995 #text_change 06-Feb-1998
C:Caccession: S56233
R:Murakami, Y: Naitou, M.: Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S:I.: Sassubmitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces
A:Acference number: S56186
A:Accession: S56233
A:Accession: S56234
A:Accession: S56234
A:Cross_references: EMBL:D50617; NID:g83668; PID:d1009858; PID:g836733; MIPS:YFL021v
A:Conetics: SCD:CANTA
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                                                                                                                                                                                                           GATKTPVVKLQNTSLYDSKIW--TTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGTLS 461
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                                                                                                                                                                                                                                                                                      640 KEDQVKQMDIENSFITK---WKDTQVSQAGDLLIEVYVERK----EPDCSIIIRISPVM 691
                                                                                                                                                                                                                                                                                                                                                         EICKLSN---KFNSVIPVRSG------HEDLE------LLD-----LSAP--- 491
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                  KOKAPOOYRIRA-----KLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDL----DIIFQD 403
LKSFLSDIDDALLTK---ELYPYWISALDTQDDKERIKKYGA-FIRSLPGVNRATLAAII 584
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                                                                                                                 Indels 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 510;
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C.Superfamily: GATA-type zinc finger homology
C.Keywords: transmembrane protein: zinc finger
F.14-30/Domain: transmembrane *status predicted <TMl>
F;307-360/Domain: GATA-type zinc finger homology <GZF>
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17.6%; Pred. No. 0.95;
tive 59; Mismatches 132;
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Matches 86; Conservative
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Lybothetical protein KIAA0580 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T00342
R;Nagsae, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1938
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: 214086; MUID:98290545
A;Reference number: 214086; MUID:98290545
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary;
A;Residues: 1-1044 < NMG>
A;Residues: 1-1044 < NMG>
A;Coss-references: EMBL:AB011152; NID:93043683; PIDN:BAA25506.1; PID:93043684
C;Genetics:
A;Note: KIAA0580
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Best Local Similarity 24.5%;
Matches 46; Conservative 26
       C;Genetics:
A;Gene: CESP:F57C2.3
A;Map position: 2
A;Introns: 115/3; 198/2
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TWY resistance protein N - tobacco (Nicotiana glutinosa)
C; Species: Nicotiana glutinosa
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C; Accession: A54810
R; Whitham, S.; Dinesh-Kumar, S.P.; Choi, D.; Hehl, R.; Corr, C.; Baker, B.
Cell 78, 1101-1115, 1994
A; fitte: The product of the tobacco mosaic virus resistance gene N: similarity to tol
A; Reference number: A54810; WUD: 95007759
A; Accession: A54810
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1144 < WHI>
A; Cross-references: GB: U15605; NID: 9558886; PIDN: AAAS0763.1; PID: 9558887
C; Genetics:
A; Gene: N
A; Introns: 160/2; 525/3; 616/3 1139/3
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3.7%; Score 122; DB 2; Length 1144;
Best Local Similarity 18.2%; Pred. No. 1.1;
Matches 135; Conservative 106; Mismatches 200; Indels 300;
                                                                        3.7%; Score 122; DB 1; Length 560;
Similarity 18.7%; Pred. No. 0.36;
12; Conservative 78; Mismatches 168; Indels 198;
F;36-43/Region: nucleotide-binding motif A (P-loop)
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Best Local Simi
Matches 102;
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A:Note: lost Excerichia coli
A:Note: lost Excerichia coli
C:Date: 17-Mar-1987 **sequence_revision 21-Nov-1997 **text_change 19-Jan-2001
C:Date: 17-Mar-1987 **sequence_revision 21-Nov-1997 **text_change 19-Jan-2001
C:Accession: A40298; T10162
R:Cram, H.; Ruger, W.
EMBO J. 4, 257-264, 1985
A:Title: Genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genomic organization as A:Title: Genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genomic organization as A:Title: Genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genomic organization as A:Reference number: A91016; MUD:85257446
A:Reference number: A91016; MUD:915229; PIDN:CAA25545.1: PID:9577852
A:Residues: 1-560 < GRA>
A:Residues: 1-560 < GRA>
A:Cross-references: GB:X01804; NID:915229; PIDN:CAA25545.1: PID:9577852
A:Residue: 16
C:Genetics:
A:Gene: 46
A:Start codon: GUG
C:Superfamily: phage T4 exonuclease 46
C:Superfamily: phage T4 exonuclease; hydrolase: nucleotide binding: P-loop
                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 HCQQIKIGEDISVDYFLKKSGSRYNFLTHAHSDHYRGLDKKWTRSVYC-----SPETAK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 LLPHIMGYTADSPPPAGLINPLE------ENVPHKFDSFQVILVNANHCPGAVMFVF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 VPVDFRNEAFQIFKRRVESVLEAVTDCDNFIEFQQKENVVQSETSTQTSSSNTSGDADLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 RCQQLSA-----TILT----DH-----QYLERIPLCAILKQKAPQQYR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 IRAKLRSY-----KPRRLFQSVKLHCPKCHLLQEVPHE-------GDLDIIF 401
                                                                                                                                                                                                                                                                                      122 YENFTTEDHKMVE-----ALRVWASTHMSPSWTLLKLCDVQPMQYFDLT-----CQL-- 168
                                                                                                                                                                                                                                                                                                                                  71 YFDVLAQVHSVVETKNGSWTLRVWRAQKFGPEASKEK----REMNLFHVTENTFKCYIVP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNHVHVARSLKVGSFLRIYSLH-----TKLQSMNSENQTMLSLEFHLHGGTSYGRGIRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 LPES--NSDVDQLKKDLESA-----NLTANQHSDVICQSEPDDSFPSSGSVSLYEVE 327
                                                                                                                                                                                                                                                                                                                                                                                                169 ----LGKA-EVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVY 223
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 EGSKIEEIAGGAVICTGDFRADKMFLESLKPGNQLHWMTE----IKFGIIYLDNTYFSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 -----ELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIP-SSVAEALGIV
                                                                                                                                                                                                                                         Indels 233;
                                                                                                                                                                                          Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 LPLSNEC----LLLIEGGTLSEICKLSNKFNSVIPV-RSGHEDL-----
                                 C;Genetics:
A;Gene CESP: 19942.1
A;Map position: 1
A;Introns: 42/3; 104/2; 160/3; 273/2; 317/2; 429/2; 502/2
                                                                                                                                                                                    Query Match 3.9%; Score 130.5; DB 2; Best Local Similarity 18.9%; Pred. No. 0.089; Matches 109; Conservative 72; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 PLOYVFVMTFTLDDGTGVLEAYLMDSDKFFQIPASE 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 MLYYTF-----GNGV-----NDDEGIIRIPYSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 PDPRIGRAVEESGREFL-------
           Experimental source: clone F39H2
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	VNVVFFSQNFE
C:Superfamily: Schizosaccharomyces hypothetical protein SPAC26H5.06	Qy
y Match 6.0%;	129 LEPKVENEDGINNYFSYTPYNFSGKSFTQEGHETKILKDLKKWSKDYFSNNDVVEQVKKA
<pre>Best Local Similarity 23.1%; Pred. No. 5.4e-07; Matches 109; Conservative 83; Mismatches 177; Indels 103; Gaps 23;</pre>	155 DVQPMQYFDLTCQLLGRAEVDGASFLLKVWDGTRTPFPSWRVLIQDL
FKPPYLS-K	189 DIETAMKNKIDFDLLARVIEISDNEUTINIVSLNDSIGGIWIGHLEKKKFPH
D5 18 KKNTIVNLFGIVKDFTPSRQSLHGTKDWYTTVYLWDPTCDTSSIGLQIHLFSKQGNDLPV 77	OY ZOZ VLEGDLSHITHKLONLTIDILOYDNHYHVARSLKVGSFLRIYSLHTKLOSMNSEN ZSS ::: : : : : : : : :
72 IYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPRTS	
O INGVOCELLENGII EKSIKUKIQESKUÇE KIALMPUFSSNSKUTLÇEÇEMPKLMKIĞUK 13/	RESULT 4 \$35525 '
OY 120SKYFNETTEDHKWAEALKWASTHAS-PSWTLLKLCDVQPMQYFDLTC 165 Db 138 FEDFALILIAKIWAEFILSTSKARDNOFILSTSKASKONOFILSTSKANOFILSTSKANOFILSTSKANOFILSTSKASKONOFILSTSKANOFILST	telomere-binding protein - Euplotes crassus C.Species: Euplotes crassus C.Date: 13-13-13-1005 #ecquision 13-13-1305 #toxt chang 07-1000
167 OLICEARUDASCELERARADESmpdpmpvir.toni.urgan.cura.out	C. Accession: 33525
198 OVI-RTWYSDRNETLYVTDYTENELFFPMSPYTSSSRMRGPFGRF 241	Nucleic Adds Res. 20. 651-6629, 1992 A.Title: Euplotes crassus has genes encoding telomere-binding proteins and telomere-!
-LKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGR 273	A;Reference number: S35524; MUID:93126105 A;Accession: S35525
DD 242 SIRCILWDEHDFYCRNYIREGDYVVMKNVRTKIDHLGYLECILHGDSARRYNM 294	A:Status: preliminary A:Molecule type: DNA
KDLESANLTANOHSDVICQSEPDDSFPSSGSVSLY 324	A;Residues: 1-460 <wan> A;Cross-references: EMBL:M96819; NID:g159025; PID:g159026</wan>
Db 295 SIEKVDSEEPELMEIKSRKRLYVQNCONGIEAVIEKLSQSQQSENPFIAH 344	C:Genetics: A:Genetic code: SGC9
AKLRSYKPRRLFQS 377	A:Introns: 18/3; 3/7/3 C:Keywords: DNA binding: nucleus
DD 345 ELKQTSVNEITAHVINEPASLKLTTISTILHAPLQNLLKPRKHRLRVQVVDFWPKSLTQF 404	
378 VKLHCPKCHLLQEVPHEGDLDIIFQDGATKIPVVKLQNISLYD 42	Overy Match 4.9%; Score 163.5; DB 2; Length 460; Best Local Similarity 21.6%; Pred: No. 000021; Matches 117; Conservative 74; Mismatches 195; Indels 155; Gaps 24;
DD 4US AVESUPPESTVWMFALLVKDVSNV-TLPVIFFDSDAAELINSSKIOPCNLAD 455	Qy 9 YIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQT-NVKLTC 59
PESULT 3	
telomere-binding protein, 51K - Euplotes crassus C.Species: Funjotes crassus	Oy 60 LLFSGNYEALPIIYKNGDIVRFHRLKIQVYKETGGITSSGFASLTFEGTLGAPI 114
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-Dec-1999 C:Accession: 535524	Db 79 ALGSRKFEDLPIIQRCGDIIRVHRAEYN-YKDDQHYFKLNMSYSSSWALFSADEEVAPEV 137
R:Wang, W.: Skopp, R.: Scofield, M.: Price, C. Nucleic Acids Res. 20, 6621-6629, 1992	115 IPRTSSKYFNPTTEDHKMVEALRVWASTHMSPSWTLLKLCDVOPMQYFD
A:Title: Euplotes crassus has genes encoding telomere-binding proteins and telomere-bind A:Reference number: S35524; MUID:93126105	138 IKDEGDDFTYRSYAYSGKQYNFDTQDQKLLKNTRAWNKSYFAKNDV 18
A: Accession: S35524 A: Status: preliminary	164 LTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVY
A Residues: 1-46 GRANA	104 TI DEMI I PENGRANGESTE NAVENATOT VINCENTA
A.Cenetic rode. GGC9	Cy 224 DNHYBYARSLANGGSLEKII SLAIAKASANDENQIMLSLEKHLANGGSISIGKALKV 2// 1 - - - - - - - - - -
A.Introns: 9/3	
C:Keywords: DNA binding; nucleus	Qy 278 LPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVER 328
Query Match 4.9%; Score 164; DB 2; Length 446; Best Local Similarity 23.8%; Pred, No. 0.00018;	329 COOLSAIILIDHQYLERIPLCAILKOKAPOOYRIRAKLRSYKPRRLFOSVKLHCPKCH
NY TYTPI, NOT K CATTUNIV COVINE PROPERTY SECTION OF	Db 312VLATTTFGDYSELPLTELSEIFEDVTDKDAVFRARFSILKITPDRVEDYVEBYTPK 367
11 HYQYSDLSSIRKEGEEDQYHFYGVVIDASFPYKGEKRYVVICKVADPSSVAKGG	387 LLQEVPHEGDLDIIFQDGATKT-PVVKLQNTSLYDSKIWT-TKNQKGRKVAV
QY S7 LTCLLFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAP 113	UD 368GRAFISKPVIKVQFLIKDPSIALNDNLIKIILLISHGULGKEFF 409 Ov 437 HEVKNNGTLDISCHFLILLIFGGTISETCKISNKFNSVIDVRSGHEDLETLDISAPFLIOG 496
- 	4.57 AT YNNNG LLFLONEC LLLFLOGG LLOGIL ALLANDYN FNO Y LYNG AELL LLDGAFF LALG

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                                                                                                                                                                                                                                                                                         1773 tcctccaggaataaaaattgatgcatatccgtggttggaatgcttcatcaagtcatacaa 1832
                                                           1653 aacaggagtactagaagcctatctcatggattctgacaaattcttccagattccagcatc 1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (EIM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF58257 standard; DNA; 936 BP
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17-MAR-2000; 2000US-0190259.
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Length 936;

1. Similarity 1.0%; Score 129.2; DB 22; Similarity 1.0%; Pred. No. 9.6e-26; B; Conservative 491; Mismatches 289;

Query Match Best Local Similarity Matches 8; Conserv

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cagaagactatttcagtctgttaaacttcattgccctaaatgtcatttgctgcaagaagt 1172
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                                                                             tccacatgagggcgatttggatatattttcaggatggtgcaactaaaaccccagttgt
                                                                                                                  caagttacaaaatacatcattatatgattcaaaaatctggaccactaaaaatcaaaagg
                                                                                                                                                                                                    НИИМЕНИЕННЕННЕННЕННЕННЕННЕННЕННЕННЕННЕН В
                                                                                                                                                                                                                                                                                                                             tctacttttgatagaaggaggtacactcagtgaaatttgcaaactctcgaacaagtttaa
                                                                                                                                                                                                                                                                                                                                                                       9, 2002, 22:18:34
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Job time: 7653 sec
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                           Sequence 475 BP; 191 A; 70 C; 69 G; 145 T; 0 other;
    Claim 25; SEQ ID No 7970; 654pp; English.
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Additionally, May be used to produce the colon cancer associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and ABB77789 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1884
                                                                                                                                                                                                                                                                                                                                                                                        ccagcatcagaagttctgatggatgatgaccttcagaaaagtgtgggatatgatcatggat 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #7970 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                     missing at time of publication, meaning no sequence listing were SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                        Length 675;
                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                     Sequence 675 BP; 213 A; 103 C; 128 G; 229 T; 2 other;
                                                                                                                                                                                                                                                                                                    'Match 10.6%; Score 201; DB 22; Local Similarity 100.0%; Pred. No. 1.2e-45; Les 201; Conservative 0; Mismatches 0;
                                                                                                                                   present invention. N.B. Pages 666 to 682 and page 7053 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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2000US-0207456.
2000US-0608408.
2000US-0532366.
2000US-0234687.
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
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Best Local S:
Matches 201;
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                                                                                                          1140 tcattgccctaaatgtcatttgctgcaagaagttccacatgagggcgatttggatataat 1199
                                                                                                                                                                                                                  Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to a composition comprising two nucleic
                                                                                                                                                                 310 tcatttcattgccaataattttaggcaagaagttccacatgagggcgatttggatataat 369
                                                      Gaps
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                                                      ö
     DB 22; Length 475;
                                                      Indels
                                                                                                                                                                                                                                                                                                                               1260 ttcaaaaatctggaccactaaaaatcaaaaaggacgaaaagtagca 1305
                                                                                                                                                                                                                                                                                                                                                            430 ttcaaaaatctggaccactaaaaatcaaaaaggacgaaaagtagca 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electron-transfer group; ETM; mismatch; genotyping;
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Score 143.6; DB 22;
Pred. No. 7.4e-30;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CLIN-) CLINICAL MICRO SENSORS INC
Ouery Match 7.5%;
Best Local Similarity 91.6%;
Matches 152; Conservative (
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17-MAR-2000; 2000US-0190259.
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of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprises a 3'-end sequence, where the oligonuclectide which comprises a 1'-end sequence, where the combination of the 5'-end sequence, sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the etection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13628 and AAH13633 to AAH13612 represent human cDNA sequences; and AAH13629 to AAH13632. The present human mino acid sequences; and AAH13632. The present human mino acid sequences: and AAH13632 to AAH13632.
          (b) a combination
      comprises at least 15 nucleotides; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
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28-JUL-2000; 2000EP-0116126

Homo sapiens. EP1074617-A2. 07-FEB-2001.

Sequence 568 BP; 167 A; 115 C; 96 G; 178 T; 12 other;

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3;
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                                                                                                                        1411 aatagtgtaattootgtgagatotggocacgaag--acotggaacttttggacotttcag 1468
                                                                                                                                                                                                                                                1469 caccatttcttatacaaggaacaatacatcactatggatgtaaacagtgttctagtttga 1528
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                                                                4;
      Length 568;
                                                             Indels
   Score 419; DB 22;
Pred. No. 6.1e-106;
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                                                          0; Mismatches
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   22.0%;
93.2%;
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Query Match 22.0
Best Local Similarity 93.2
Matches 465; Conservative
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comparises: (a) an oligo-dT primer and an oligonoucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence of oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide comprises a 1-and sequence complementary to a polynucleotide comprises a 1-and sequence which comprises and sequence oligonucleotide comprises a 1-and sequence which comprises and sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers also useful for the connection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and ANISAS and ANISAS and ANISAS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer*** for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 2182; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                ogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-HAY-2000; 2000JP-0241899.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   Ota I,
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                                              1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                            agattocagcatcagaagttotgatgatgatgaccttcagaaaagtgtggatatgatca 1759
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tggatatgttttgtcctccaggaataaaaattgatgcatatccgtggttggaatgcttca
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer) SEQ ID NO:2138.
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Sugiyama T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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02-MAY-2000;
09-JUN-2000;
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27-AUG-1999;
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 -end sequence; where the oligonucleotide comprises at 3-end sequence the comprises at least 15 nucleotides and the combination of the 5-end sequence/3-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13613 to AAH18631 represent human cDNA sequences, AAB92446 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                      Length 576;
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                                                                                                                                                      Sequence 576 BP; 167 A; 113 C; 114 G; 173 T; 9 other;
                                                                                                                                                                                    Score 545; DB 22;
Pred. No. 9.1e-141;
0; Mismatches 7;
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Matches 545; Conservative
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Yang Y,
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u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                       nucleic acids and polypeptides, useful is central nervous system injuries -
                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1484; 10078pp; English.
                                                                                                                                                                                                 Xu C,
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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                                          2000US-0552117-
2000US-0552117-
2000US-058042-
2000US-0620312-
2000US-0653450-
2000US-0663191-
2000US-0663191-
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P-PSDB; AAM40125.
                                                                                                                                                                                                         Zhou P,
                                                                                                                                                           (HYSE-) HYSEQ INC
                                           21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-A:7G-2000;
14-SIEP-2000;
19-OCT-2000;
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99.8%; Score 1901.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1903; Conservative 0; Mismatches 251 301 191 121 311 241 371 61 181 g g ó ga O g ŏ à ద ò

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detection; diagnosis; antisense therapy; gene therapy;

CDNA sequence SEQ ID NO:17112

(first entry)

2000EP-0116126

2000JP-0183767

BP.

2383

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Primer sets for synthesizing polynucleotides, particularly t
full-length cDNAs defined in the specification, and for the
and/or diagnosis of the abnormality of the proteins encoded
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
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      AAH17603 standard; cDNA;
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                                                                                                                                                                                                         full-length cDNAs
                                                    Human; primer;
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                                                                Homo sapiens.
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                             26-JUN-2001
                                                                                       07-FEB-2001.
                 AAH17603;
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                cagtatttggagagacaccactatgtgccattttgaaacaaaaagctcctcaacaatac
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sogai T, Nishikawa Sugiyama T, Wakama

Isogai T,

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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set (ull-length cDNAs defined in the specification. Where a primer set to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotides sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the following the following sequence complementary to the comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence is nucleotides and the complementary to a polynucleotide comprises a 1-east 15 nucleotides and the complementary to a polynucleotide sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the complementary without any specialised methods. AAR03166 to AAR13628 and AAR03631 to AAR13631 to AAR13632 to AAR13632 to AAR13632 to AAR13632 to AAR13633 to AAR13633 to AAR1364 to AAR1364 to AAR13640 to AAR13660 to AAR1
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        English.
8; SEQ ID 17112; 2537pp + CD ROM;
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full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 8; SEQ ID 11187; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligord T primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the ombination of the 5'-end sequence(3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers also votaining of the full-length cDNAs. The primers are also waseful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the AMH13613 to AMH13613 to AMH13613 to AMH13613 to AMH13614 to AMH13618 and AMH13613 to AMH13614 thuman amino acid sequences; and AMH13629 to AMH13612 represent luvention.

Sequence 2631 BP; 826 A; 473 C; 491 G; 841 T; 0 other;

; tttcacaggetgaagattcaagtatataaaaaggagactcagggtatcaccagetetgge 300 360 503 aagtattttaacttcactactgaggaccacaaaatggtagaagccttacgtgtttgggca aagtattttaacttcactactgaggaccacaaaatggtagaagccttacgtgtttgggca ctaaaggtatgggatggcaccaggacaccatttccatcttggagagtcttaatacaagac Length 2631; ; Indels 22; DB 100.0%; Score 1905; 100.0%; Pred. No. 0; Mismatches .; 0 Best Local Similarity 100. Matches 1905; Conservative Query Match -144 204 241 264 301 324 361 384 444 481 541 61 421 84 181 g ò g ô පු οy g õ οp õ 윱 ò 셤 ò 占 å g ò

1140 900 960 863 gtalenattatacgaggtagaaagatgtcaacagctatctgctacaatacttacagatcat gtatcattatacgaggtagaaagatgtcaacagctatctgctacaatacttacagatcat tttcåggatggtgcaactaaaaccccagttgtcaagttacaaaatacatcattatatgat tcaaaaaatctggaccactaaaaatcaaaaaggacgaaaagtagcagttcatttgtgaaa gaagacctggaacttttggacctttcagcaccatttcttatacaaggaacaatacatcac gaagacctggaacttttggacctttcagcaccatttcttatacaaggaacaatacatcac aaaacatcgtggattccttctgtggcagaagcactgggtattgtacccctccaatat tttcaggatggtgcaactaaaaccccagttgtcaagttacaaaatacatcattatatgat tcaaaaatttggaccactaaaaatcaaaaaggacgaaaagtagcagttcattttgtgaaa aataatggtattccccgctttcaaatgaatgtctacttttgatagaaggaggtacactc tatggatqtaaacagtgttctagtttgagatccatacaaaatctaaattccctggttgat aaaacatcgtggattccttcttctgtggcagaagcactgggtattgtacccctccaatat atctatagccttcataccaaacttcaatcaatgaattcagagaaatgttaagt ttagagtttcatcttcatggaggtaccagttacggtcggggaatcagggtcttgccagaa ttagagtttcatcttcatggaggtaccagttacggtcggggaatcagggtcttgccagaa agtaactctgatgtggatcaactgaaaaaggatttagaatctgcaaatttgacagccaat 1044 1104 1141 1201 1224 1284 1321 1344 1404 1441 1464 1501 1621 661 684 781 804 864 901 924 961 984 1021 1081 1164 1261 1381 564 601 721 g ŏ g ò Op ò op ò Q ò g ò g ò QQ ò g ò Op ò g ò ö a 9 ò g ò g ò

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The present sequence represents module 8 of the FK-520 polyketide synthase (PKS) gene cluster of strain MA6548. FK-506 is a potent final consuppressants, and acts through intial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide compounds are used as immunosuppressants to prevent or treat transplant rejection, graft-verus-host disease or uveitis. They can also be used for treating e.g. alopecia universalis, autitiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurite outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and sclatic nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and contains a
                                                                                     Example 2; Page 90-93; 125pp; English.
peripheral neuropathy
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1574 AA; Sequence

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                                                                                                                                                        212 RLQNLTIDILVYDN - - - HVHVARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGG 268
                                                                                                                                                                                                                                 269 TSYGRGIRVLPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVER 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 AVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLS-APFL 493
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Ouery Match 3.2%; Score 105.5; DB 21; Length 1574; Best Local Similarity 21.9%; Pred. No. 2.2; Matches 92; Conservative 44; Mismatches 160; Indels 125; Gaps
                                                                             167 QLLGRAEVDGA-----SFLLKVWDGTRIPFPSWRVLI----QDLVLEGDLSHIH 211
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PR 16-JUL-1999; 9905-0144086.

PR 19-JUL-1999; 9905-0144312.

PR 19-JUL-1999; 9905-0144313.

PR 19-JUL-1999; 9905-0144313.

PR 21-JUL-1999; 9905-0144313.

PR 22-JUL-1999; 9905-0144314.

PR 21-JUL-1999; 9905-0144814.

PR 21-JUL-1999; 9905-0144814.

PR 21-JUL-1999; 9905-0144814.

PR 22-JUL-1999; 9905-0144814.

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PR 22-JUL-1999; 9905-0145086.

PR 22-JUL-1999; 9905-015086.

PR 23-JUL-1999; 9905-015086.

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22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 FSGNYEALPIIYKNGDIVRFH---RLKIQVYKKETQGITSSGFASLTFEGILG--APIIP 116
                                                                                                                                                                                                                                                                                                                                                                                                               The CDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The CDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit CPSII while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 RISSKYFNFTI ---- EDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLICQLLGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 INYITTPLNQ--LKGGTIVNVYGV--VKFFKPPYLSKGTDYCSVVTIVDQINVKLT-CLL
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                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding carbamoyl phosphate synthetase II - isolated from Plasmodium falciparum, used to develop prods. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4%; Score 114; DB 15; Length 2391;
21.0%; Pred. No. 0.67;
ve 85; Mismatches 235; Indels 108;
                                                                                          "carbamoyl-phosphate-synthase domain"
        "glutamine-amidotransferase domain"
                                                                                                                "ATP binding subdomain CPSa"
                                                                                                                                                           'note⇒ "ATP binding subdomain CPSb"
                                                                      "glutaminase subdomain"
                             "structural subdomain"
                                                                                                           /note= "ATP binding subd
1255..1857
/note= "insert sequence"
1858..2391
                                                 "insert sequence"
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Matches 114; Conservative
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16-DEC-1992;
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fungal resistance; verticillium wilt; vascular disease; transgenic plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a tomato verticillium polypeptide. The polypeptide is encoded by Vel.1 and Vel.2 resistance genes. The polypeptide confers resistance to Verticillium species in a plant. Verticillium are fundi, which cause verticillium wilt in plants. This is a common vascular diseases that causes sever yield and quantity losses in many crops. The polypeptide is useful for producing a transgenic plants that are resistant to Verticillium species.
                                                                                                                                                                                                                                                                                                                           1296 nnnnn-----mnsgnvenkcklnkesygynnssncintnniniennic----hdisinkn 1346
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                                                 DLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATI--LIDHQYL----
                                                                                                                           344 ERTPLCAILKOKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQD
                                                                                                                                                                                                                                                              GATKTPVVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEI
                                                                                                                                                                                                                                                                                                                                                                                                 464 CK--LSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTIHHYGCKQCS-----SLRSIQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a verticillium (Vel.1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verticillium polypeptide; Vel.1; Vel.2; resistance gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kulcsar F;
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(REGC) (USDA) Baker BJ WPI; 199 N-PSDB; Plant vi generati Virus Example The Nico resistan coding f library protein resistan	Sequence Ouery Match Best Local Matches 13 71 IIY	125 FTT 388 161 XFD 438 f1d 438 f1d 482 yng 272 GRG 539 sst 321 595 1km 329 655 1ee 655 1ee 655 1ee 714 eige 773 less 447 LSN	
2	XX S S O O O M		oy ob
		AAR88122 standard; Protein; 1144 AA. AAR88122; 28-MAR-1996 (first entry) 28-MAR-1996 (first entry) Tobacco mosaic virus resistance N gene protein. Tobacco mosaic virus resistance; TWV: N gene; Solanaceae; crop improvement; transgenic plant; crop improvement. Nicotiana glutinosa. Key Location/Qualifiers 1150 /label= Cytoplasmic_region /label= P-loop /note= ArP/GTP-binding site motif* Binding-site 228229 /label= P-loop /note= ArP/GTP binding site motif* Binding-site 297302 /label= P-loop /note= ArP/GTP binding site motif* S90928 /label= Leucine-rich_region /note= "ArP/GTP binding site motif* S90928 /label= Leucine-rich_region /note= "ArP/GTP binding site motif* /label= Leucine-rich_region /note= "ArP/GTP binding site motif* /note= "ArP/GTP binding site motif* /label= Leucine-rich_region /note= "ArP/GTP binding site motif*	.1995. 1995, 95WO-US07754. 1994; 94US-0261663.
193 tsa 235 VGS 208 295 ANL 232 355 KAP 254 415 NTS 272 475 PVR	320 ps 535 IV 371 de 593 pG 422 -9	302	W09535024-A1 28-DEC-1995. 16-JUN-1995; 17-JUN-1994;
0	6 6 6 6 6 B	### A X X X P X B X F F X S X F E E E E E E E E E E E E E E E E E E	XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLICQLLGKAEVDGASFLLKVWD-----GTRIPFPSWRVLIQDLVLEGDLSHIHR 212
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| mlvhlqlrhnslrhlwtetkhlpslrridlswskrltrtpdftgmpnleyvnlygcsn 654
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                                                                                                                                                                                 irus resistance gene N sequences from tobacco - useful for ing transgenic Solanaceous plants resistant to Tobacco Mosaic
                                                                                                                                                                                                                                                                                                             octiana glutinosa N gene protein (AAR88123) mediates ince to tobacco mosaic virus (TMV). The gene (AAT09341) for the protein was obtd. from a N. glutinosa leaf genomic / by screening with a cDNA clone. DNA sequences encoding the n can be used to generate transgenic plants, esp. Solanaceae, int to TMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFTLDDGTGVLEAY-LMDSDKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 3.7%; Score 122; DB 17; Length 1144; Similarity 18.2%; Pred. No. 0.03; S.; Conservative 106; Mismatches 200; Indels 300;
                                                                                                                                                                                                                                                                           6; Page 52-60; 98pp; English.
UNIV CALIFORNIA.
                                                                    J, Whitham SA;
                                                                                                               96-058144/06.
AAT09340.
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Matches

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 75533.
               AAG58505 standard; Protein; 467 AA.
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9905-0130891
9905-01310891
9905-0132048
9905-0132485
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99US-0130077.
99US-0130449.
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990S-0139456.
990S-0139457.
990S-0139458.
                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                  99US-0126785
                                                                  (first entry)
                                                                                                                                            termination sequence
                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                           EP1033405-A2.
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
06-APR-1999;
08-APR-1999;
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ID AAG5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                    Peptide #8301 encoded by probe for measuring placental gene expression.
                                                 Gaps
                             Gaps
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   Length 66;
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                           Indels
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96.7%; Pred. No. 1.9e-07;
tive 0; Mismatches 1;
ch 10.8%; Score 358; DB 22; Score 358; DB 22; St. 1 Similarity 100.0%; Pred. No. 1.1e-27; 66; Conservative 0; Mismatches 0;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023659.
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Matches 29; Conserv
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Query Match
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                                                                                                                                                        MSLVPATNYIYTPLNQLKGGTIVNVYGVVRFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL
                                                 RIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPVVKLQNTSLYD
                                                                                                                                                                                                             KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL
                                                                                                                       LKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLR
                                                                                                                                                  IYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTAN
                                                                                                                                                                                                                               SKIWTTKNOKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGH
                                                                                                                                                                                                                                                         EDLELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQY
                                                                                                                                                                                                                                                               VEVMTFTLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFCPPGIKIDAY
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                  634;
                  Length
                               Indels
                  22;
                               1;
                  DB
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                       Pred. No. 0;
0; Mismatches
                  Score 3317;
Pred. No. 0;
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                 99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
               Query Match
Best Local Similarity 99.8
Matches 633: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer;
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                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                     AAB93478;
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comptises: (a) an oligo-dT primer and an oligounclectide complementary
to the complementary strand of a polynuclectide comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonuclectide comprises at least 15 nucleotides; or (b) a combination
of an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence of the complementary to a
polynucleotide which comprises a 1'-end sequence, where the
oligonucleotide comprises a 1'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers also useful for the
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH136131 to AAH13612 represent human cDNA sequences; and AAH13629 to AAH13612

represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                                                                                                                         nikawa I, Hayashi K, Saito K, Y
Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 12761; 2537pp + CD ROM; English
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                sogai T, Nishikawa
Sugiyama T, Wakama
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02-MAY-2000; 2
09-JUN-2000; 2
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Gaps 1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFL 22; DB Score 3317; DB Pred. No. 0; Mismatches 99.8%; Matches 633; Conservative Similarity Best Local

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IYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQLKKDLESANLTAN LKVWDGTRTPFPSWRVL1QDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLR QHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATILTDHQYLERTPLCAILKQKAPQQY

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                                                                                                                                                                     Q9C2K8 PRELIMINARY; PKI; '>> AA.
Q9C2K8;
Q1-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
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isolate, host-silkworm, Genomic, 6542 nt].";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033596; BAA85362.1; -.
Nonstructural protein.
SEQUENCE 1115 AA; 128304 MW; 7C0DA2DCFA746428 CRC64;
                                                                                        Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
    Schulte U.,
                           SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICO-SEPDDSFPSSGSVSLYEVERCQQLSATI----LTDHQYLERTPLCAILKQKAPQQYR
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J.,
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Matches
                                                                                                                                                          SEQUENCE FROM N.A.

Llaca V., Lou A., Messing J.W.;

Llaca V., Lou A., Messing J.W.;

Microsynteny analysis of 22-kDa zein cluster in massing in the cluster in massing in the cluster in massing in the cluster in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
SERINE-TYPE CARBOXYPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl.
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ da
EMBL; AL513442; CAC28643.1; -
SEQUENCE 759 AA; 85218 MW; DC737A5574FF4F73
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Submitted
                                                                                                                     Carboxypeptidase.
SEQUENCE 483 AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9XE80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPSWR---VLIQDLVLEGDLSH--IHRLQNLTIDILVYDNHVHVAR--SLKVGSFLRIYS
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                        Similarity
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                                                                                                                       53413 MW;
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the EMBL/GenBank/DDBJ databases
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                      Score 110.5; D
Pred. No. 0.57;
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Pred. No. 0.
                                                                                                                       DB91DCCEF772A0D9 CRC64;
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STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
MEDLINE-98069011; PubMed-9405937;
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Sequence features of the regions of 1,044,062
Physically assigned P1 clones.*;
DNA Res. 4:291-300(1997).
EMBL; AB006700; BAB08933.1; -.
SEQUENCE 463 AA; 53630 MM; A735DBF109155D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots: Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana (Mouse-ear cress).
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Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                         VNVYGVVKFFKPPYLSKGTDYCSVVTIVD--QTIVKLTCLLFSGNYEALPIIYKNGDIVR
                                         FHRLKIQVYKKETQGI----TSSGFASLTFEGTLGAPIIPRTSSKYFNFTTEDHKMVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIRVLPESNSDVDQLK--KDLESANLTANQHSDVICQS-----EPDDSFPSSGSVSLY
  LSRVKIVLINRKITALCNETTSSSEA--LFNGKHSVDSIPYQSSPKFLMREQDKNFLSNL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVLSQPPSSYVWMFALLVRDVSNV-TLPVIFFDSDAAELINSSKIQPCNLAD
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                                                                                 VNLIGVIVELG --- FSNGSDCSCTLKIVDPWYSGSGLPVKFVARTIRDLPRVES: GDIIL
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Last annotation updat
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01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence up
01.JUN-2001 (TrEMBLrel. 17, Last annotation
ALPHA TELOMERE BINDING PROTEIN.
Oxytricha trifallax.
Cukaryota: Alveolata; Ciliophora: hypotrichs
Oxytrichidae; Oxytricha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prescott J.D., DuBois M.L., Prescott D.M.;
"Oxytricha trifallax macronuclear alpha telomere bindingene.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF067831; AAC27615.1;
HSSP; P29549; 10TC.
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                                                             HLRTGEVVRIRSATYDETSTQKKVLLLSHYSNIVTFISTSKLAK--ELRGKITDDRAVEK
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                                                                                                                                                                                                                                                                                                               NSDYATLVLYAKRFEDLPIIHRLGDIIRIHRATIRLYNGQRQFNANIFYSSSWALFSTDK 153
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Search completed: April 9, 2002, 17:08:56
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; LIBRARY: LVZNN
; CLONE: 348429
US-09-274-570-3
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US-08-323-170B-2
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                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             APPLICANT: Williamson, kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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             CLASSIFICATION: 424
RIOR APPLICATION DATA:
                                             APPLICATION NUMBER: US/08/323,170E
FILING DATE: 13-OCT-1994
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APPLICATION NUMBER:
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Two Embarcadero Center, 8
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19.5%; Pred. No.
US 08/010,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 3; Length 425; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 175;
                                                                                                                                                                                                                                                  l and Crew LLP
8th Floor
                                                                                                 #1.30
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                                                                                       RESULT 14
US-08-310-912A-108
: Sequence 108, Application
: Patent No. 5981730
: GENERAL INFORMATION:
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            APPLICANT:
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APPLICANT:
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US-08-323-170B-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: P-41, 261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                      1196
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1298 RVNK-----TFDENVEYTCNIKIENFFNYI 1322
                                                                                                                 1253 IKQVVK---KIKVIITKNDTVLLKREVQSESTLDDKIYKCEHE-
                                                                                                                                                                                                                                                                                                                                                  1136 KIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1055 SLGKLLNFLDTQET-----VCLTEKI------RYLNLSINELGSDNNT-FSVTFQV 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000 NTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYK----NHKDVKYFEQSSVLSPLSSAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 YEALPIIYKNGDIVRFH------RLKIQVYKK--------ETQGITSSG-
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GTIVN----VYGV----VKFFKPPYLSKGTDY------CSVVTIVDQTN-VKLTCLLFSGN
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                                                                                                                                                                                                                                   QPENCFNNVYKGLNSVDITTILKN---AQTYNINNKKTPTFLKIPPYNLLEDVEISC-QCT 1252
                                                                                                                                                                                                                                                                                              QLSATILTDHQYLERTPLCAILKQKAPQQYRIRAK----LRSYKPRRLFQSVKLHCPKCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPYIDIKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSFLRIYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDVDQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKV
                                                       LSNECLLLIEGGTLSE----IC--KLSNKFNSV 473
                                                                                                                                                                         LLQEVPHEGDLDIIFQDGATKTPDVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILP
                                                                                                                                                                                                                                                                                                                                                                                                            -----KKDLESANLTANQH-----SDVICQSEPDDSFPSSGSVSLYEVERCQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTEDHKMVEA---LRVWASTHM------SPSWTLLKLCDVQPMQYFDLTCQLLGKAEVD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FASLTFEGTL-----GAPIIPRT------SSKYFNF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEEL-----NFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
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Ausubel, Frederick M

US/08310912A

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Dahlbeck, Douglas Katagiri, Fumiaki Brent, Andrew Staskawicz, Brian

Kunkel, Barbara N

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.4%; Score 93.5; DB 2; Length 1461; Best Local Similarity 21.3%; Pred. No. 4.4; Matches 76; Conservative 51; Mismatches 118; Indels 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Renneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    105 TFEGTLGAPIIPRTSSKYENF-----TTEDHKMVEALRVWASTHMSPSWTLLKLCDVQ 157
                                                                                                                                                                                                                              624
                                                                                                                                                                                                                                                                                                                                                                  158
                                                                                                                                                                                                                                                                                                                                                                                                          531 TLDGT-----PRTLNTVFDFPPPPLDQVQEEECEVERV----TEHGTP------K 570
                                                                                                                                      680
                                                                                                                                                                                                                                                                        218 IDILYYDNHVHVARSLKV--GSFLRIYSLH-----TKLQSMNSENQTMLSLEFHLHGGTS 270
                                                                                                                                                                                                                                                                                                                     571 PFRKFDSVA--FGESQSEDEQF----ENDLETDPPNWQQLVSREVLLG-LKPCEIKRQEV 623
                                                                                       322 SLYEVERCOOLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKPRRLF2SVKLH 381
382 CPRCHLLQEVPHEGDLDI/IFQDGATKTPDVKLQNTSLYDSKIWTTKNQKGRKVAVH 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/993,228
                                                                                                                                                                                                                                                                                                                                               PMQYFDLTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLT 217
                                                                                                                                    QMKAVRKRNET-SVIDQIGEDL----LTWFSGPGEEKLKHAAATFCSNQP------F 725
                                                                                                                                                                                 YGRGIRVLPESNSDVDQLKKDLESANLT------ANQHSDVICQSEPDDSFPSSGSV 321
                                                                                                                                                                                                                              INELFYTERAHV-RTLKVLDQVFYQRVSREGILSPSELRKIFSNLEDILQLHIGLN---E 679
                                          ALEMIKSRQKKDSRFQTFVQDAESNPLCR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : (617) 876-5851
(617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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US-08-951-148-3
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Patent No. 587
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                           LIBRARY: LYL-
175
                                                                                                125
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CITY: Palo Alto
                                                                                                                                  76
                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                   16 LSLSGHVGFDSLPDQLVNKSTSQGFCFNILCVGETGIGKSTLMDTLFNTKFESDPATHNE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                               FTTEDHKMVEAL-----RVWASTH-MSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGA 177
                                                                                                                                  PGV----RLKARSYELQESNVR----LKLTIVDTVGFGDQINKDDSYKPIVEYIDAQFEA 127
                                                                                                                                                                  GDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLG------APIIPRTSSKYFN 124
                                                                 YLQEELKIKRSLFNYHDTRIHACLYFIAPTGHSLKSLDLVTMKKLDS----
                             SFLLKVWDGTRTPFPSWRVLIQDLVLEGDL --- SHIHRLQNLTIDILVYDNHVHVARSLK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                     LVZNNOT01
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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KVNIIPIIAKADTIAKNELHKFKSKIMSELVSNG----
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                                                                                                                                                                                                                                                                    Indels 124;
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 208
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22;

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; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-458-791-2
                                                                                                                                                                                                                                      RESULT 6
US-09-459-066-2
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TELEPHONE: (206)470-4189
TELEFAX: (206)23-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                   APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 KDTEGRSLATQELGRLKLCEGAGSLHFVDAFLWNGSIYFPYYP-----YNYTS-----
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                                CITY: Seattle
                                                    ADDRESSEE: Janis C. Henry STREET: 51 University St.
 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                      TGYCTP----PICV 512
                                                                                                                                                                                                                                                                                                                                                                                         RHSKCMVK-NVDSSRELCQNKSQPNRTCTCSIPTRATYKDVSVVNVMFSFGSWNLSDRFN 588
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                                                                                                                                                                                                                                                                                                                   FTNCSSLKECPACV 602
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Pred. No. 3
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
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589 FINCSSLKECPACV 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                       IGYCIP----PICV 512
                                                                             RHSKCMVK-NVDSSRELCONKSOPNRTCTCSIPTRATYKDVSVVNVMFSFGSWNLSDRFN 588
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                                                                                                                                                                                                                                       YKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTATDPHCGWCHSLQRCTFQGD 486
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                                                                                                                                                                                                                                                                              -----CAILKQKAPQQYRIR-AKLRSYKP-RRLFQSVKLHCPKCHLLQEVPHEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 3.5%; Score 94.5;
1 Similarity 20.0%; Pred. No. 3
99; Conservative 60; Mismatch
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                                                                                                                                                                                  -----LDIIFQDGATKTPDVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILP 446
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Gaps

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RESULT 7 US-09-308-375-2 ; Sequence 2, Application US/09308375

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US-09-150-741-2
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                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09150741 Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                               LENGTH: 2
TYPE: PRT
                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                             939
                                                                                                                               y Match
3.9%; Score 106; DB 4; Length 2391;
Local Similarity 20.9%; Pred. No. 0.52;
hes 109; Conservative 80; Mismatches 230; Indels 19
  62
                                                                                        7 THYIYTPLNQ--LKGGTIVHVYGV--VKFFKPPYLSKGTDYCSVVTIVDQINVKLI-CLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -IDWDE--KKIIEELKNPSPK-RIDAIHQAFHLNMPMDKIHELTHIDYWFL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CK--LSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTIHHYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSATI--LTDHQYL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNYEYYKFREIALKVITHLNIIGECNIQFGINPQTG---EYCII----EVNARLSRSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHDVLPLNMKRK------KICTLNNKRNANKKKVHV-KNHLYNEVVDDKDTQLHKEN
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FSGNYEALPIIYKNGDIVRFH---RLKIQVYKKETQGITSSGFASLTFEGTLG--APIIP 116
                                             SNYEYYKFREIALKVITHLNIIGECNIQFGINPQTG---EYCII-----EVNAFLSRSSA 990
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; MOLECULE TYPE: US-08-264-002-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08264002 Patent No. 5559019 GENERAL INFORMATION:
                                                                                                                       TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1197
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                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GUI, JIAN-PANG
APPLICANT: FU, XIANG-DONG
TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
NUMBER OF SEQUENCES: 17
                                                                                                  SEQUENCE CHARACTERISTICS
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CITY: L
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                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                               REGISTRATION NUMBER: P-38,347
                                           TOPOLOGY:
                                                                                                                                                            TELEPHONE:
                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHDVLPLNMKRK-----KICTLNNKRNANKKKVHV-KNHLYNEVVDDKDTQLHKEN 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IDWDE--KKIIEELKNPSPK-RIDAIHQAFHLNMPMDKIHELTHIDYWFL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASKATGYPLAYISAKIALGYDLISLKNSITKKTT--
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California
                                                           amino acid
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                                                                                655 amino acids
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                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                 Version
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|--ACFEPSLDYITTKIP
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PRINTS; PR00020: MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM00031; FA58C; 2.
SMART; SM00137; MAN; 1.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRP1_XENLA STANDARD; PRT; 928 AA.

P28824;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

NEUROPILIN-1 PRECURSOR (A5 PROTEIN) (A5 ANTIGEN).

Xenopus laevis (African clawed frog).

Zenaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91337458; PubMed-1908252;
Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fuj.
"The A5 antigen, a candidate for the neuronal recognition
DOMAIN
DOMAIN
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DISULFID
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                                                                                                                                                                                                                                                                                                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
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                                                                                                                                                                  CHAIN
                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000859; CUB.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D10467; BAA01260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has homologies to complement components and coagulation
                                                                                                                                      TRANSMEM
                                                                                                                                                   DOMAIN
                                                                                                                                                                                        Antigen.
                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEURONS.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ron 7:295-307(1991).

FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CURCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVINESTY. PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITIC DETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
 1
22
22
861
884
27
147
275
275
431
646
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 21
928
860
883
928
141
265
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424
584
812
542
104
                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CUB 1.
CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
 PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
                                                                                                                                            POTENTIAL.
NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                       Neurone;
                                                                                                                                                                                                        signal;
                                                                                                                                                                                                        Repeat;
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CARBOHYD
SEQUENCE
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CARBOHYD
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                    437
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                                                                                                                                                                                                                                                                                         TEDHKMYEALRVWA----STH-MSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVDGASFLL 181
                                                                                                                                                      IRV-LPESNSDVDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLS
                    H 437
                                                                                       WAVLNSKTGPVQDH-----TGDGNFIYSEADERHEGRA-----ARLMSPVVSSSRSAH
                                                                                                                                 LTVGATGQSTETPTVEASPEEPDMT---HSDLDCKF----GWGSQKTVCNWQHDISSDLK
                                                                                                                                                                               GFIRIIPERASASGLALRLELLGCEVETPTSIPTTPEVNGGDECEGDLANCHSGTDEGFK
                                                                                                                                                                                                 SFLRIY-----FHLHGGTSYGRG
                                                                                                                                                                                                                          KFKIGYSNNGTEWEMIMDSSKNKPKTFEG-----NTNYDTPELRTFAHITT----
                                                                                                                                                                                                                                                KVWDGTRTPFPSWRVLI-----QDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVG
                                                                                                                                                                                                                                                                                                                   -----PVTWENGISLRFELYGCKITDYPCSRMLGMVSGLISDSQITASSQVDRNWV
                                                                                                                                                                                                                                                                                                                                        IQVYKKETQGITSSGFASLTFE-------GTLGAPIIPRTSSKYFNFT 126
                                           CLTFWYHMDGSHVGTLSI---
                                                               CPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQNTSLYDSKIWTTKNQKG-----RKVAV
                                                                                                                                                                                                                                                                     PELARLYTSRSGWALPPSNTHPYTKEWLQIDLAEEKIVR----GVIIQGGKHKENKVFMR
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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431
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261
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928
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1 584
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                                                                                                           DHQYLERTPLCAILKQKAPQQYRIRAKLRSYKPRRLFQSV-----KLH
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BY SIMILARITY.
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                           Score 97.5; DI
Pred. No. 12;
69; Mismatches
                                          ---KLKYEMEEDFDQTLWTVSGNQGDQWKEARVVL
                                                                                                                                                                                                                                                                                                                                                                                                                    97.5;
No. 12;
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CRC64;
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Search completed: April 9, 2002, 17:11:19 Job time: 248 sec

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Matrix protein; Pho
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                                                                                                            PPE1_HUMAN STANDARD: PRT; 653 AA.
014829; 015253; Q9UJH0; Q9NU21;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
50-AUG-2001 (Rel. 40, Last annotation update)
50-AUG-2001 (Rel. 40, Last annotation update)
50-AUG-2001 (Rel. 40, Last annotation update)
60-AUG-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 MAMOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1996)
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                                        PPEF1 OR PPEF OR PPP7C.
Homo sapiens (Human)
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVVQLPKNKIDYHSTFFLPENEVNRQNGVQSRDQLSKNSTNDLQKILELRERIKTIKQNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGSEDGLLSSVKK-----DSMILDEPRNSTSINNSKKMHRILQTEILDLTDQTMHRPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTPEPIQTFKVLTDLSKSSLSNQFESSSKKTSHGSSFNPEPF--IKTEQRSNNTLSKDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LIEGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSSTRTLNMIGTNDV---NASMKEKESASSAKKNQLVKDVKWTPSSSLLDLSRRNDLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATK-----TPDVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLS--NECLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDIFKLPSEKRRKEIVHENLQSFDDE------HNEMSLPPQDQKSIKQKNGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KAPQQYR----IRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U43400; AAC54672.1; -.
x protein; Phosphorylation
NCE 755 AA; 86580 MW; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IAVAPDGINQVIDTLSKLDLHNSNKVIDIVSSPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLV
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InterPro;

IPR002048; IPR000048;

EF-hand.

Ser_thr_phosphtse

300109;

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Montini E., Rugarli E.I., van de Vosse E., Andolfi G., Mariani M., Puca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; *A novel human serine-threonine phosphatase related to the Drosophila retinal degeneration C (rdgC) gene is selectively expressed in sensor; neurons of neural crest origin. *; Hum. Mol. Genet. 6:1137-1145(1997).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: MAY HAVE A ROLE IN THE RECOVERY OR ADAPTATION RESPONSE OF PHOTORECEPTORS. MAY HAVE A ROLE IN DEVELOPMENT. MAXIMAL ACTIVITY IS OBSERVED AT PH 8.0.
-I- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang X., Honkanen R.E.;
*Molecular cloning, expression, and characterization of a novel human serine/threonine protein phosphatase, PP7, that is homologous to prosophila retinal degeneration C gene product (rdgC).*;
J. Biol. Chem. 273:1462-1468(1998).
                                                             EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
HSSP;
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Submitted (
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degeneration C.";
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"Identification and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Retina;
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                                                                                                                                                                                                                                                                                                              ENTYME REGULATION: ACTIVATED BY CALCIUM.

ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1 (SHOWN HERE), 1A, 1B, 2

ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 3 MAY HAVE NO FUNCTIONAL SIGNIFICANCE.

TISSUE SPECIFICITY: DETECTED IN RETINA AND RETINAL DERIVED RETINOBLASTOMA CELLS. ALSO FOUND IN FETAL BRAIN.

SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.

SIMILARITY: CONTAINS 1 IQ DOMAIN.

SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: MAGNESIUM.
                                                             AF027977; AAC05825.1; 294056; CAB40074.1; -. AL096700; CAB86407.1; P08129; IFJM.
                                                                                                                                 AF023455; AAB82795.1; -. X97867; CAA66461.1; -.
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H., Macke J.P.,
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CC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION
CC PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS
CC SUGH AS LAWININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT
CC SUBSTRATE FOR CELLS.
CC I. SUBCHIT: PURIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE IN
CC SUBCELULAR LOCATION: EXTRACELLULAR.
CC I. SUBCELLULAR LOCATION: EXTRACELLULAR.
CC I. TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC I. PIN: CONTAINS THE HEPRAN SULFATE CHAINS AS WELL AS N-LINKED
CC I. SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC I. SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
CS SIMILARITY: CONTAINS 3 LAMININ DOMAINS.
CC I. SIMILARITY: CONTAINS 3 LAMININ DOMAINS.
                                                                                                                                                                     Pfam: PF00008;
Pfam: PF000057;
Pfam: PF000053;
Pfam: PF000054;
Pfam: PF000054;
Pfam: PF000054;
Pfam: PF000100;
PFAM: PF00010010;
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PFAM: PF000100180;
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                                                                                                                                                     Signal;
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                                                                                                                                                                                                                                                                                                     $M00180;
$M00001;
$M00408;
$M00281;
$M00282;
$M00192;
$M00200;
                                                                                                                                Basement membrane;
sulfate; Laminin EC
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PS50068;
PS50024;
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PS01186;
PS01248;
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J IPR000742; EGF_2.
J IPR001438; EGF_II.
J IPR003006; Ig_MHC.
J IPR003598; Ig_c2.
J IPR002172; LDL_recept_A.
J IPR0000034; Laminin_B.
IPR002049; Laminin_EGF.
J IPR0001791; Laminin_G.
J IPR000082; SEA.
                                                                                                                                                              0303; Laminin_B; 3.
180; EGF_Lam; 6.
01; EGF_like; 8.
08; IGC2; 22
31; Lam6; 3.
2; LDLa; 4.
2; SEA; 1.
12; EGF_l; 9.
86; EGF_2; 5.
48; LAMININ_TYPE_EGF; 1
19; LDLRA_1; 4.
4; SEA; 1.
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AAB21121.2; -.
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                                                                                                              matrix; EGF-like
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EGF-like domain;
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BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN.

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24.1%;
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LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

IG-LIKE C2-TYPE DOMAIN 1.

LAMININ DOMAIN IV 1 (DOMAIN III A).

LAMININ DOMAIN IV 1 (DOMAIN III A).

LAMININ EGF-LIKE 1

LAMININ EGF-LIKE 3

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 7

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

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IG-LIKE C2-TYPE DOMAIN 1.

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P51979;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                         YEAST
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                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                               HFM1 PROTEIN.
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STRAIN-S288C / FY
                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSGRYECMLVLYPEGIQTKIYNLLIQTHVTADEW-NSNHTIEIEINQTLEIPCFQNSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMOWSKVTNKIDLIAVYHPQY----GFYCAYGRPCESLVTFTETPENGSKWTLHLRNMSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNLT--ID-ILYDNH--VHVARSLKVG--SFLRIYSLHTKLQS---MNSENOIMLSLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KY----FNFTTEDHKMVEALRVWASTHMSPSWTLLK------LCDVQPMQYFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FSGNYEALPITYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPITPRTSS
                                                                                                                                                                                                                                                                                                                                                                                                PATSSVTLVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFSCHIRVGPNKILRSSTTVKVFAKPEIP-----VIVENNSTDVLVERRFTCLLKNVFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LTCQL-LGKAEVDGASFLLKVWDGTRTPFPSWRVLIQ----DLVLEGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KISSEFTYAWSVEDNGTQETL--ISQNHLISNSTLLKDRVKLGTDYRLHLSPVQIFDDGR
                                                                                                                                                                                                                                                                                                                                                                                                                PSSGSVSLYEV
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ALSPYPGNKYWNISSEKITFLLGSEISSTDPPLSYTE-STLDTQPSPASSYSPARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLHGGTSYGRGIRVLPESNSDVD-QLKKDLESAN--LTANQHSDVICQSEPDDS-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANITWFIDGSFLHDEKEGIYITNEERKGKDGFLELKSVLTRVHSNKPAQSDNLTIWCM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                    (MAR-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 110.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                 1048
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                                                                                                                VITRO
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      RAN PAR
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EMBL: Z7Z///,

EMBL: Z7Z///,

R GD: S000320; HFM1.

R GD: S000320; HFM1.

R InterPro: IPR001410; DEAD.

R InterPro: IPR001650; Helicase_C.

DR Pfam: PF00270; DEAD: 1.

DR Pfam: PF00270; DEAD: 1.

DR SMARR: SM00487; DEXDC: 1.

DR SMARR: SM00490; HELICC: 1.

KW Nuclear protein: Zinc-finger; DNA-binding; Helicase; ATP (POTENTIAL).

FT NP_BIND 20 27 ATP (POTENTIAL).

FT SITE 127 413 MISSING (IN REF. 2).

TRING 900 915 C4-TYPE (POTENTIAL).

TRING 900 915 C4-TYPE (POTENTIAL).

TRING 900 915 MISSING (IN REF. 2).

TO TAKE TO THE TOTAL SABBESTF625D4758 CRC6
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                                                                                                                                                                                                                                                                                         RESULT
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Best Local Similarity
                                                                                                                                                  P39846:
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seque
20-AUG-2001 (Rel. 40, Last annot
PEPTIDE SYNTHETASE 2.
PPSB OR PPS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: U22156: AAA93159.1;
EMBL: x94357; CAA64136.1;
EMBL: Z72773; CAA96971.1;
SGD: S0003220; HFM1.
                                                                              Bacillus subtilis.
Bacteria: Firmicutes: Ba
Bacillus/Staphylococcus
NCBI_TaxID=1423:
MEDLINE=95227362; PubMed=7711903;
Tognoni A., Franchi E., Magistrelli
                                                                                                                                                                                                                                                         PPS2_BACSU
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                                 STRAIN=168;
                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNGIKI ---- KNDISLLPCLNIRTKLENCKI - ENEELWLTFKVEISATFKSSIWHGQHLS
                                                                                                                                                                                                                                                                                                                                                                             KCHLLQEVPHEG-----DLDIIFQDGATKTPDVK-----LQNTSLYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               YEVERCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKPRRLFQSVKLHCP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRGIRVLPESNSDVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSLNGHCWENTPMVLRQLKTIGLVSVRRLIRHGITNLEEMGHLSDT--QIEYYLN--LKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FPSYEGASKLHOTLVODKFLV--FRHCFRLLKCMVDTFIEKSDGTSLKNTLFLL 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGTRTPFPSW-----RVLIQDLVLEGDLSHIHRLQNLTIDILV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMVEALRVWASTHMSPSWTLLK---LCDVQPMQYFDLTCQ---LLGKAEVDGASFLLKVW ::: ::| | | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTFEGTLGAPIIPRTSSKYFNFTTEDH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTFFYVRFGKNPAAYQEVNRYVSFHSVEDSQINQFCQYLLDTLVKVKIIDISNGEYKSTA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NEKKLFKEINLSP----LLKYPFLTEKKQSQIIDRVSQKVSLLIQYELGGLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                LDIE--TEKSSGELIDFRRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YDNHVHVARSLKVGSFLRIYSL--H--TKLQSMNSENQTMLSLEFHLHGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GNAMTRHYISFESMK---QFINAKKFLSL--QGILNL----LATSEEFSVMRVRH
                                                                                                                                                                                                                                                                                                                                              -QEIAGLGKTIVYSTDHLASQFSAKTPNIRKDLNSLEKCLFYES
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                                                 Z
A
                                                                                                                                                                                                                                                         STANDARD;
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21.2%;
                                                                                                     Bacillus/Clostridium group;
us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QLKKDLESANLTANQHSDVICQSEPDDSFPSS--
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                                                                                                                                                                                       sequence update)
annotation update)
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Pred. No. 2.4;
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   с.
С.
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   Colombo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161;
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     Cosmina
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29;

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GATI_YEAST
ID GATI_Y
ID GATI_Y
ID GATI_Y
ID GATI_Y
ID 101-NOV
IT 01-NOV
IT 0
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P43574;
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coffman J.A., Rai R., Cunningham T., Svetlov V., Cooper T.G.; "Gatlp, a GATA family protein whose production is sensitive to nitrogen catabolite repression, participates in transcriptional activation of nitrogen-catabolic genes in Saccharomyces cerevisiae."; Mol. Cell. Biol. 16:847-858(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
TRANSCRIPTIONAL REGULATORY PROTEIN GAT1.
                                                         PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
PROSITE; PS50114; GATA_ZN_FINGER_2; 1.
Transcription regulation; DNA-binding; Zinc-finger; Nuclear zn_FING 310 334 GATA-TYPE.
                                                                                                                                                                                                                                SGD; S0001873; GAT1.
InterPro; IPR000679; ZnF_GATA.
Pfam; PF00320; GATA; 1.
                                                                                                                                                                                                                                                                                                                     EMBL; U27344; AAB03516.1;
EMBL; D50617; BAA09217.1;
HSSP; P17429; SGAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAT. Genet. 10:261-268(1995)

1: FUNCTION: POSITIVE REGULATOR OF MULTIPLE NITROGEN

1: SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

1: SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami Y., Naitou M., Hagiwara H., Shibata T., Oz
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E.,
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAT1 OR YFL021W
      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C / AB972;
MEDLINE-95400292; PubMed-7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96182087; PubMed=8622686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
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                                                                                                                                                                            SM00401; ZnF_GATA; 1.
      510 AA;
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E., Yokoyama
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P04522;
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                                                        Gram H., Rueger W.;
"Genes 55, alpha gt, 47
organization as deduced
EMBO J. 4:257-264(1985).
                                                                                                                                                                                              Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G Mesyanshinov V., Ruger W., Stidham T., Thomas E.; Bacteriophage T4 genome analysis "; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=85257446; PubMed=4018026;
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  FUNCTION: EXONUCLEASE INVOLVED IN F
REPLICATION, AND REPAIR.
SUBUNIT: CONSISTS OF TWO SUBUNITS:
SIMILARITY: STRONG TO T5 PROTEIN DI
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0 (Rel. 13, Last sequents)
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E SUBUNIT 2 (EC 3.1.1)
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Q1-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 20:6621-6629(1992).
-I- FUNCTION: MAY BIND TELOMERIC T4G4 SEQUENCES.
-I- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-I- SIMILARITY: BELONGS TO THE TELOMERE-BINDING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93126105; PubMed=1480483;
Wang W., Skopp R., Scofield M., Price C.;
"Euplotes crassus has genes encoding telomere-binding telomere-binding protein homologs.";
"Lelomere-binding protein homologs.";
"Lelomere-binding protein homologs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 01-JUN-1994 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR03415; Telo_bind_alpha.

Pfam; Pf02307; Telo_bind_alpha; 1.

PfAm; Pf02307; Telo_bind_alpha; 1.

DNA-binding; Nuclear protein; Telomere; Multigene family.

SEQUENCE 460 AA; 53360 MW; EDIC141385A0B5FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M96819; AAA29128.1; -. PIR; S35525; S35525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euplotes crassus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELOMERE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
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                                                                                                                                                                                                                                                                     YIYTPLNQL--KGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQT-NVK-----LTC
LTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLIIDILVY
: | | | | | : | : : | | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVKGDVLRIKSVSAKEDNSLIFSSHSNILK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQSMNSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVQPMQY----FDLTCQLLGKAEVDGASFLLKVWDGT------RTPFPSWRVLIQDL
                                                                                                                                                       ALQSRKFEDLPIIQRCGDIIRVHRAEYN-YKDDQHYFKLNMSYSSSWALFSADEEVAPEV
                                                                                                                                                                              LLFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGIT----
                                                                                                                                                                                                                                         YETTEIGSIEEENEASINFYAVVIDACFPYKVDEKKYMCYLKVIDITHNVKEGDDNFAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEPRVENEDGTNNYFSYTPYNFSGRSFTQEGHETKILKOLKKWSKDYFSNNDVVEQVKKA
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                                                                  IKDEGDDFTYRSYAYSGKQYNFDTQDQKLLKNTRAWNKSYFAKN-----
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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29,
29,
                                                                                       -RTSSKYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQFMQYFD
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Pred. No. 0.00
74; Mismatches
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ches 196;
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92249771; PubMed-1577273; Mitcham J.L., Lynn A.J., Prescott D.M.; *Analysis of a scrambled gene: the gene alpha-telomere-binding protein in Oxytri Genes Dev. 6:788-800(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDILINE-92035001; PubMed-1840510; Gray J.T., Celander D.W., Price C.M., Cec *Cloning and expression of genes for the protein: specific subunit interactions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-ARY-2000 (Rel. 39, Last annotation update)
TELOMERE-BINDING PROTEIN ALPHA SUBUNIT (TELOMERE-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Alveolata; Ci
Oxytrichidae: Oxytricha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDA SUBUNIT) (TEBP ALPHA).
MAC-56A AND MAC-56S
                                                                                                                                                                                                                                         "Crystal structure of the Oxytricha nova complexed with single strand DNA.";
                                                                                                                                                                                                                                                                                     Horvath M.P.,
Schultz S.C.;
                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE=99091054; PubMed=9875850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 67:807-814(1991).
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  STRANDED TELOMERIC OVERHANG. MAY ALSO PARTICIPATE IN TELOMERE LENGTH REGULATION DURING DNA REPLICATION. BIND SPECIFICALLY TO THE TAGA-CONTAINING EXTENSION ON THE 3'STRAND AND PROTECT THIS REGION OF THE TELOMERE FROM NUCLEASE DIGESTION AND CHEMICAL MODIFICATION. SUBGUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. SUBCELLULAR LOCATION: NUCLEAR.
MISCELLULAR LOCATION: NUCLEAR.
MISCELLANEOUS: THE SEQUENCE OF THE A (OR ALANINE) VERSION IS SHOWN. THE S (OR SERINE) VERSION DIFFERS IN ONLY TWO POSITIONS, AND THE K VERSION IN ONLY ONE. THERE MAY BE OTHER VERSIONS IN
                                                                                                                                                                           1 95:963-974(1998).
FUNCTION: MAY FUNCTION AS
STRANDED TELOMERIC OVERHAN
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                                                                                                                                                                                                                                                                                                            Schweiker V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ciliophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAPRSKPYYKVQFLIKDPSTALNDNLYKIYLYSHGDLGKEFF-
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                                                                                                                                                                              PROTECTIVE CAPPING OF THE SINGLE-
NG. MAY ALSO PARTICIPATE IN TELOMERE
                                                                                                                                                                                                                                                                                                            Bevilacqua
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he Oxytricha telomere-binding
in the telomeric complex.";
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                                                                                                                                                                                                                                                                  end binding
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56

455

409

protein

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RESULT 12
1700342
hypothetical protein KIAA0580 - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00342
R:Nagase, T:; Ishikawa, K:; Miyajima, N.; Tanaka, A.; Kotani, H.: Nomura, N.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX
A:Reference number: Z14086; MUID:98290545
A:Accession: T00342
B:Citatue: T00181
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A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-1044 <NAG>
A:Cross-references: EMBL:AB011152; NID:g3043683; PIDN:BAA25506.1: PID:g3043684
A:Experimental source: brain; clone HJ0601
C:Genetics:
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Best Local S
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Local Similarity 20.2%;
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                                                                                                 KQKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEG--DLDIIFQDGATKTPD
                                                                                                                                                                                                            PIIVNSCIAFVTQYGLGCKYIYQKNGDPLHISELLESFKKDARSFKLRAGKHQLEDVTAV
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                                 VKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGTLSEICKLSNKF
                                                                                                                                          LKSFLSDIDDALLTK----ELYPYWISALDTQDDKERIKKYGA-FIRSLPGVNRATLAAII
                                                                                                                                                                         ----QSEPDDSFPSSGSVSLY------EVERCQQLSATILTDHQYLERTPLCAIL
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Pred. No. 3.4;
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                                                                  KC---SEINHMNAHNLALVF-----
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 SSCLFQTKGQTSEEVNVIEDLI 630
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RESULT T18410

carbamoyl-phosphate synthase (glutamine-hydrolyzing)
C:Species: Plasmodium falciparum

(EC

6.3.5.5)

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malaria

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hypothetical protein F26D2.10 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 20-Jun-2000 C:Accession: T21403 R:McMurray, A.
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A:Introns: 29/1; 568/2; 608/3; 746/1; 871/3; 910/1; 985/1; 1018/3; 1124/1; C:Superfamily: Caenorhabditis elegans hypothetical protein F36D3.5
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A;Gene: CESP:F26D2.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone F26D2 C; Genetics:
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A;Cross-references: EMBL:281513; PIDN:CABO4180.1; GSPDB:GN00023; CESP:F26D2.10
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A;Accession: T21403
A;Status: preliminary: translated from GB/EMBL/DDBJ
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Matches 110; Conserv
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                                                                                                                   TDHQYLERTPLCA---ILKQKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQE----
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LIEHGADLTLL--NTLNKTPEQMIPLDSPDNSKDKIEKLEKIRKL---YNKANG
                         - VPHEGDLDIIFQDGATKTPDVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNG 443
                                                                              LDNQDGKNTLLDAVREINKTNVMKAVKLGSYITAYNK---FGNTALHAATKSALPEIVKI
                                                                                                                                                            FPWIYILLICIGSILLIGLFCVVAYGFTKNGRAKYTNLYLYYFGKPLDYERRWRYS--LF
                                                                                                                                                                                               FP-----SSGSV-------SLY------EVERCQQLSATIL 337
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RESULT 7

$56233

probable membrane protein YFL021w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 06-Feb-1998

C:Accession: $56233

R;Murakami, Y; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanumitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces cells. Pacession: $5623

A;Accession: $5623

A;Accession: $5623

A;Accession: $5623

A;Accession: $5623

A;Cross-references: EMBL:D50617; NID:g836685; PID:d1009858; PID:g836733; MIPS:YFL021w

C;Genetics:

A;Gene: SGD:GAT1

A;Cross-references: SGD:S0001873; MIPS:YFL021w

A;Map position: 6L

C;Superfamily: GATA-type zinc finger homology

C;Reywords: transmembrane protein; zinc finger

F;14-30/Domain: transmembrane #status predicted <TM1>
F;307-360/Domain: GATA-type zinc finger homology <GZF>
exonuclease 46 (EC 3.1.11.-) chain 2 - C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 17-Mar-1987 #sequence_revision
C;Accession: A04298; T10162
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                                                                                                                                                                                                SGHEDLELLDLSAP----FLIQGTIHH
                                                                                                                                                                                                                                   SLKTDIIKKRQRSSTKINNNITPPPSSSLNPGAAGKKKNYTASVAASKRKNSLNIVAPLK
                                                                                                                                                                                                                                                                                                                                       --KTPDVKLQNTSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNEC--LLLIEGGT--L
                                                                                                                                                                                                                                                                                                                                                                                                           ILKQKAPQQYRIRAKLRSYKPRRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFENVFDDDDDDDDVETHS;VHSDLLNDMDSASQRASHNASGFPNFLDTSCSSSFDDHFI
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                                                                                                                                                                                                                                                                                                        TSSNPDIRCSNCTTSTTPLW-RKDPKG-----
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Pred. No. 0.15
54; Mismatches
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                    21-Nov-1997
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                                                                                                                                                                                                                                                                                                      - LPLCNACGLFLKLHGVTRPL
                #text_change
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R:Gram, H.; Ruger, W.
EMBO J. 4, 257-264, 1985
A; Title: Genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genes 54, Alpha-gt, 47 and 46 of bacteriophage T4: the genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genes 63; A; Reference number: A91016; MUID:85257446
A; Recession: A04298
A; Accession: A04298
A; Collective: DNA
A; Residues: 1-560 <GRA>
A; Cross-references: GB:X01804; NID:915229; PIDN:CAA25945.1; PID:95
A; Note: the authors translated the initiation codon GUG for residue C; Genetics:
A; Genetics:
A
                                                                                                             hypothetical protein F57C2.3 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C:Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *t C;Accession: T22839 R;Baynes, C.
submitted to the EMBL A; Reference number: Z1 A; Accession: T22839 A; Status: preliminary;
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                                                                                                                                                                                                                                                                                              9
preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIQDLVLEGDLSHIHRLQNLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQ-SMNSEN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKGQLINSTNKKELLVE---LW----
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                                                                                                                                                                                                                                                                                                                                                                                FSYASFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTDMLKDSGIKGAIIKKYIPLFNKQINHYLKIMEA---DYVFTLDEEFNETIKSR-GRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSA-----KPRRLEQSVKL- 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQNTSLYDSKIWTTKNQKGRKV 434
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Z19624
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   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 118; DB
Pred. No. 0.36;
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R:Wang, W.: Skopp, R.: Scofield, M.: Price, C.
Nucleic Acids Res. 20, 6621-6629, 1992
A:Title: Euplotes crassus has genes encoding telomere-binding proteins
A:Reference number: S35524; MUID:93126105
A:Accession: S35525
                                                                                                                                                                                                                                                              telomere-binding protein - Euplotes crassus
C;Speckes: Euplotes crassus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S35525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Wang, W.; Skopp, R.; Scofield, M.; Price, C.
Nucleic Acids Res. 20, 6621-6629, 1992
A:Title: Euplotes crassus has genes encoding telomere-binding
A:Reference number: $35524; MUID:93126105
A:Accession: $35524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomere-binding protein, 51K - Euplotes crassus
C:Species: Euplotes crassus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1~460 <WAN>
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A;Molecule type: DNA
A;Residucs: 1-446 <WAN>
A;Cross-references: EMBL:M96818; NID:g159023;
A;Genetic code: SGC9
A;Introns: 18/3; 377/3
C;Reywords: DNA binding;
                                                          A;Cross-references: EMBL:M96819; NID:q159025; PID:q159026
C;Genetics:
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A; Introns: 9/3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 IIPRT----SSKYF------NFTTEDH--KMVEALRVWASTHMSPSWTL--LKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 HYQYSDLSSIRKEGEEDQYHFYGVVIDASFPY--KGEKRYVVTCKVADPSSVAKGGKLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVLSOPPSSYVMMFALLVRDVSNV-TLPVIFFDSDAAELINSSKIQPCNLAD 455
                                                                                                                                                                                                                                                                                                                                                                                                                             LVKGDVLRIKSVSAKEDNSLIFSSHSNILK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLEGDLSHIHRLONLTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLOSMNSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVQPMQY----FDLTCQLLGKAEVDGASFLLKVWDGT-----RTPFPSWRVLIQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNVVFFSQNFEDLPIIQRVGDIVRVHRARLQHYNDAKQLNVNMYYRSSWCLFIGNDKEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTCLLFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFAS---LTFEGTLGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYIYTPLNQLK----GGTIVNVYGVVKFEKPPYLSKGTD-YCSVVTIVDQTNV-----K 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKLHCPKCH-----LLQEVPHEGDLDIIF--QDGATKTPDVKLQNTSLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIETAMKNKTDFDLLAKVTEISDNDQYTNTVSLNDSTGQTWTGHLFKRKFPH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEPKVENEDGTNNYFSYTPYNFSGKSFTQEGHETKILKDLKKWSKDYFSNNDVVEQVKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELKQTSVNEITAHVINEPASLKLTTISTILHAPLQNLLKPRKHRLRVQVVDFWPKSLTQF
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Pred. No. 7.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                           -FFSFSSIHKKLKSSISSD
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C;Species: Oxytricha nova
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_ch
C;Accession: A41221; B41221
R;Gray, J.T.; Celander, D.W.; Price, C.M.; Cech, T.R.
Cell 67, 807-814, 1991
A;Title: Cloning and expression of genes for the Oxytricha
A;Reference number: A41221; MUID:92035001
A;Accession: A41221
                                                                                                                                                                                                                                                                                                                                                                                                                                                   macronuclear alpha protein (alanine version) - Oxytricha
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                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-310,'S',312-455,'E',457-495 <GR2>
A;Cross-references: GB:M68930; NID:g159813; PID:g159814
                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-495 <GRA>
A; Cross-references: GB:M68931;
                                                                                                                                                                                                           A; Accession: B41221
                                                                                                                                                                                                                                                                                     A; Status: preliminary
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Best Local Similarity 21.4
Matches 116; Conservative
                                                                                                               Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 -----PGVDPSSAQ------TPSGHSKL-RKYASTLMKFNVHIDAVLEKVGGAFFIRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 LPESN----SDVDQLKKDLESANLTANQHSD----VICQSEPDDSFPSSGSVSLYEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 APHSNIMTFVPFSRLAKSLDSQISLSPDKVDKELIKKVILTEP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 YEYTEIGSIEEENEASINFYAVVIDACFPYKVDEKKYMCYLKVIDTTHNVKEGDDNFAIV 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DN-----HVHVARSLKVGSFLRIY-SLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTCQLLGKAEVDGASFLLKVWDGTRTPFPSWRVLIQDLVLEGDLSHIHRLQNLTIDILVY 223
                                                                                             code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQG
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; Pred. No. 0.00029;
74; Mismatches 196
Score 148.5; DB Pred. No. 0.0013;
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Best Local Similarity

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Length

Query Match

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/map="7"
/clone="RP5-1007F24"
/clone_lib="RPCI-5"
1 127
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7297. .777
                                                                                                                                                                                                                                                                             /rpt_fami
14937. .1
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9100. .9549
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8153. AGD1
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5592. .5900
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7772. .8152
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3422. .3643
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/rpt_family="Retroviral"
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                                                                                                                                                                  /rpt_family="MIR"
17371. .17552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="/
11462. .11492
                                                                                                                                      /rpt_family="MIR"
18822. .19117
                                                                                                                                                                                                                       /rpt_family="L2"
15817. .15913
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/note="match to EST AA001442 (NID:g1436973) ze45d11.s1"
21448. .21674
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    AC015911.6 GI:15148313
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32787. .32820
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24901. .24984
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21675. .21858
/rpt_family="MER1_type"
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32978. .33089
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34075. .34126
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Local Similarity 9.5%; Pred. No. 3.4;
hes 80; Conservative 316; Mismatches 4.
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Primer A: CAGAAAAGTGTGGATATG
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49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08,
Tel: 3014020201
Fax: 3014024735
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Contact: Eric D. Green
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The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
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VNLSLKNNIITLVATNRARIANQKIKTEDSQDFNLTINSKVVKELISLLSMSNTLILSP
GTFELKIKSGNLEIKTKVIEIPYMNVENVFPNKFNFVHIDKKELLSLISMSNTLILSP
KNGNKILIEYNPSKKEKKLKLSSYMPDLGFFSVFSDNFEVESBILLKFFINANYLKES
INVFDGMISIFITENKDRMVISSETNLNNKQLIAALRGH"
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similar to SWISS-PROT:P34029 (DP3B_SPICI)
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1741. .2862
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VHFFQLKKOINEFNKLTISNIFKNVEITKENTTPERIIEHVANYYKLPKHELISKSRK
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/product="CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA"
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/translation="MSKKSLDKIDLLAYNKTLODIFESKINDSMLYQNIFKFLEITKV
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MFDDFQIFSIGNKRATLNFIEBILDKBLMNNKTTLTSDKDLKFMASLFEGGLYTRLS
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/transl_table=4
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/db_xref="taxon:2107"
  /gene="MYPU_0030"
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possible; Blastp2 P=6e-47

putative; Blastp2 P

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Waterston,R.H.
Direct Submission
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Jones, K., Tin-Wollam, A. and Keppler, D. The sequence of Homo sapiens PAC clone RP5-907C10
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Submitted (22-JAN-1999)
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Center project name: H_DJ0907C10
                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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                Summary Statistics
                                                                                                                                                                                                                                                                                               Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry: an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information University Denome Sequencing Center of additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared Pieter de Jong and coworkers at the Roswell Park Cancer Institut (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is one male donor Institute is from

The clone may be obtained either from Genome Systems, (http://www.genomesystems.com) or Research Genetics, (http://www.resgen.com); or from Pieter de Jong. Inc.

NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP5-907C10;
actual end is at 154959 of RP5-907C10.

The RP5-907C10 sequence from 4689 to 5920 ıs from PCR product

FEATURES repeat_region source /clone_lib="RPCI-5" 66. .259 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7" /map="7g31-3g32" /clone="RP5-907C10" 1. .154959 /rpt_family="L1" Location/Qualifiers DNA.

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                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - 6 3'-end one pass sequencing: Departent of Virology and Human Genome Center; Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                  Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                oligo capping; fis Homo sapiens human clone: HSI02573.
                                                                                                                                                                                                                                                            Unpublished (2000)
2 (bases 1 to 1752)
Sugano, S., Suzuki, Y., Ota, T.,
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NEDO human cDNA sequencing project
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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QIPASFVLMDDDLQKSVDNIKDMFCPPGIKIDAYPWLECFIKSYNVTNGTDNQICYQI
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/clone_lib="NT2RM2"
/clone_lib="NT2RM2"
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neuronal precursor cells."
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                             gaagacctggaacttttggacctttcagcaccatttcttatacaaggaacaatacatcac
                                                                                                                                            aataatggtattctcccgctttcaaatgaatgtctacttttgatagaaggaggtacactc
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VLPESNSDUDQLKKDLESANLTANQHSDVICQSEPDDSFPSSGSVSLYEVERCQQLSA
TILTDHQYLLERTPLCAL LKQKAPQOYR HAKLRSYKPRFLGOSVKLHCPKCHLLQEVP
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LRSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFTLDDGTGVLEAYLMDSDKFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cloning vector: pME18SFL3-mRNA from
neuronal precursor cells."
439. .2343
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="teratocarcinoma"
/clone="NT2RM2001805"
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Catarrhini;
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Tissue Procurement: ArCC/DCTD/DTP
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y. Wetherby K.D. Beckstrom-Sternberg,S.M.,
Benjamin,B. Blakesley,R.M., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan, X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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Series:
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ilarity 95.3%;
Conservative
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TILTDHQYLERTPLCALLKQRAPQQYRIRAKLHSYKPRRLGSYKLHCPKCHLLGEVP
HEGDLDIIFQDGATKTPDVKLQNTSLYSSKIHTTKNQKGRKVANHFVKNNGILFLSNE
CLLLIEGGTLSBICKLSNKFNSYIPVRSGHEDLELLDLSAPFLIQGTIHYGCKQCSS
LRSJQNLNSLVDKTSHIPSSYNAEALGIYPLQYVFVMTFTLDDGTGVLEXYLMDSDKFF
QIPASEVLMDDDLQKSVDMIMDMFCPPGIKIDAYPWLECFIKSYNVTNGTDNQICYQI
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/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or a single surface -
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                        The present invention relates to single exon nucleic acid probes (SE) The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                        WPI;
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    Sequence
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analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
    475
                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                 Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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      B₽;
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                                                                                                                                                                                                                                                                                                                                                                                              2000GB-0024263
    191
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                                                                                                                                                                                                                                                                                                               DK,
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                                                                                                                                                                    7970;
    Α;
                                                                                                                                                                                                                                                                                                                 Chen
    70
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%; Pred. No. 1.1e-45;
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    69
                                                                                                                                                                                                                                                                                                               Rank
  G;
                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                 DR;
  145
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  0
  other;
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                                                                                                                                                                                                                                useful
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                                                                                                                     (SENP).
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Query

Match

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Score 146.8;

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Length 475;

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RESULT 13
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                                                                          Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 92.8 Matches 154; Conservative
                                                                                                                                                           The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
  1062
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electron-transfer group; gene expression; ss.
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                                                                                                                                                                                                                                                 Example 6;
                                                                                                                                                                                                                                                                                                                       WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF58252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58252 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                     (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2001
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                                                                                  Local Similarity
                                                                                                                                                                                                                                                                        single surface
                        tacaatacttacagatcatcagtatttggagaggacaccactatgtgccattttgaaaca 1061
aaaagctcctcaacaataccgcatccgagcaaaattgaggtcatataagcccagaagact 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttcaaaaatctggaccactaaaaatcaaaaaggacgaaaagtagca 1305
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                                                                           10;
                                                                                                                                       936
                                                                                                                                                                                                                                              Page 127; 159pp; English.
                                                                          Conservative
                                                                                                                                     B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                     4
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                                                                                                                                     139 C;
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                                                                          484;
                                                                       Score 121; DB 22
Pred. No. 1.7e-23;
84; Mismatches 29
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                                                                                                                                    7 T;
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smatches 12;
                                                                                                                                     776 other
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                                                                                              DB 22;
                                                                          299;
                                                                                              Length 936;
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                                                                         Gaps
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RESULT
AACC2802
ID AAC;
XX
AC AAC;
XX
AC AAC;
XX
DT 06-C
XX
DE Huma
XX
KW Huma
XX
CS Home
XX
SS Home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of CC oligonucleotide which comprises at sequence, where the combination of CC the 5'-end sequence's'-end sequence's rend sequence is selected from those defined in CC in gene therapy. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full length cDNAs. The primers are also useful for the cCC detection and/or diagnosis of the abnormality of the proteins encoded by CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH3633 to AAH1842 represent human cDNA sequences; AAB92446 to CC AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632 CC represent oligonucleotides, all of which are used in the exemplification could be comprised to the comprise of the complement of the complemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                                                               AAC28094 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 866 BP; 254 A; 162 C; 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present invention.
                                                                           gene
                             Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctctttagtggaaactatgaagcccttccaataatttataaaaatggagatattggtcgc
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                                                                           therapy;
                                                                                                                                                        secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
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                                                                                                        EST:
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                                                                                                                                                                                                         (first entry)
                                                                        ; expressed sequence
chromosome mapping;
                                                                                                                                                      protein 5'
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91.2%;
                                                                                                                                                           EST,
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                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342; DB 22;
No. 1.3e-84;
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                                                                                                        secreted
                                                                                                                                                           32169
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                                                                                                     protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
              Query Match
Best Local Similarity
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
331;
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID 32169; 71pp + CD-ROM; English.
                                                                                     336 BP; 108
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9905-0122487
                17.7%;
                                                                                   A; 70
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              Score 321.8; DB:
Pred No. 3.3e-79
                                                                                       69 G;
   Mismatches
                                                                                       86
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                                                                                       T; 3 other;
                                   DB 21;
   Indels
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В
301
                                                                                                                                                                       937
                                                                                                                                                                                                       121
                                                                                                                                    181
                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                          cagagaatcagacaatgttaagtttagagtttcatcttcatggaggtaccagttacggtc
                 aaacaaaaagctcctcaacaataccgcatccgagc
                                                                                                                                                                                                                     aatc-tgcaaatttgacagccaatcagcattcagatgttatctgtcaatcagaacctgac
                                                                                                                                                                                                                                                                  ggggaatcagggtcttgccagaaagtaactctgatgtggatcaactgaaaaaggatttag 120
                                                                                                                                                                                                                                                                                      ggggaatcagggtcttgccagaaagtaactctgatgtggatcaactgaaaaaggatttag 877
                                                                                                                                                                                                                                                                                                                                        cagagaatcagacaatgttaagtttagagtttcatcttcatggaggtaccagttacggtc
aaacaaaaagctcctcaacaataccgcatccgagc
                                                                                  tctgctacaatacttacagatcatcagtatttggagaggacaccactatgtgccattttg
                                                                                                                                    gacagctttccaagctctggatcagtatcattatacgaggtagaaagatgtcaacagcta
                                                                                                                                                     gacagettteeaagetetggateagtateattataegaggtagaaagatgteaaeageta
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                                                                  tctgctacaatacttacagatcatcagtátttggagaggacaccactatgtgccattttg
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RESULT 10 AAH12625/c ID AAH126

AAH12625 standard;

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ВP

AAH12625

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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
to the complementary strand of a polynucleotide which comprises one of the $602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                   Claim
                                                                                                                     Primer sets for synthesizing polynucleotides, particularly t
full-length cDNAs defined in the specification, and for the
and/or diagnosis of the abnormality of the proteins encoded
full-length cDNAs -
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3, Sugiyama
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; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakamatsu
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CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB13633 to AAH18742 represent human cDNA sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification CC of the present invention.
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Sequence 576 BP; 167 A; 113 Ç 114 <u>င</u> 173 Ţ; 9 other;

Similarity

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Matches 545;
                           26-JUN-2001
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       (5'-primer)
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CDNA

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29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                      Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
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99JP-0300253.

2000JP-0118776.

2000JP-0183767.

2000JP-0241899.
                                                                                                                                                       Hayashi K,
A, Nagai K,
                                                                                                                                                       Saito K, Yamamoto J;
Otsuki T;
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 8; SEQ ID 11187; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC objected and oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence complementary to a cC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 1'-end sequence, where the CC oligonucleotide comprises a 1'-end sequence, where the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for clustering encoded by CC chapses and chapses the companion cald sequences; and AAH13628 and CC AAB13633 to AAH18742 represent human cDNA sequences; and AAH13629 to AAH13632 cof the present oligonucleotides, all of which are used in the exemplification.

Sequence 2631 BP; 826 A; 473 C; 491 G; 841 T; 0 other;

Query Match 94.4 Best Local Similarity 95.3 Matches 1814; Conservative

94.48;

Score 1713.8; Pred. No. 0; Mismatches

DΒ

Length 2631; ; 68

2; 22;

Indels

Gaps

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360	301 tttgcafctttgacgtttgagggaactttgggagcccctatcatacctcgcacttcaagc	Оу з
300	241 tttcacaggctgaagattcaagtatataaaaaggagactcagggtatcaccagctctggc 	Оу 2 рь 2
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                      assays
C.N.S (
                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral_gclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitites such as: Immune system suppression, Activinjoinhibin activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Wang
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2000US-0653450.
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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide sequence complementary to the comprises at least 15 nucleotides; or (b) a combination cofficient an oligonucleotide which comprises a 5 end sequence complementary to a polynucleotide which comprises a 5 end sequence and an oligonucleotide comprising a sequence, where the coligonucleotide which comprises at least 15 nucleotides and the combination of the 5 end sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs d
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Sequence 2077 BP; 657 A; 401 Ç; 393 G; 626 T; 0 other;

Conservative

94.5%;

Score 1717; Pred. No. 0;

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Length 2077;

Mismatches

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Best Local Similarity
Matches 1816; Conserv 611 481 551 421 191 361 431 301 371 241 311 181 251 121 191 131 19 1 atgtctttggttccagcaacaaattatatatatacacccctgaatcaacttaagggtggt 60 ctctttagtggaaactatgaagcccttccaataatttataaaaatggagatattgttcgc ctaaaggtatgggatggcaccaggacaccatttccatcttggagagtcttaatacaagac tctactcatatgtcaccgtcttggacattactaaaattgtgtgatgttcagccaatgcag tctactcatatgtcaccgtcttggacattactaaaattgtgtgatgatgttcagccaatgcag tttgcatctttgacgtttgagggaactttgggagcccctatcatacctcgcacttcaagc ttcacaggctgaagattcaagtatataaaaaggagactcagggtatcaccagctctggc acaattgtcaatgtctatggtgttgtgaagttctttaagcccccatatctaagcaaagga 250 acaattgtcaatgtctatggtgttgtgaagttctttaagcccccatatctaagcaaagga 120 atgtctttggttccagcaacaaattatatatatacacccctgaatcaacttaagggtggt 190 tttgcatctttgacgtttgagggaactttgggagcccctatcatacctcgcacttcaagc tttcacaggctgaagattcaagtatataaaaaggagactcagggtatcaccagctctggc 430 0 0; Indels 9; Gaps 480 240 670 610 550 490 360 300 370 ۲.

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RESULT 1
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Best Local
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1 (bases 1 to 782)
L1, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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AL520360
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                                                                                                                                                                                                                                                                                                                 /note=*Organ: brain; Vector: pCMVSPORT 6: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com*

http://fulllength.invitrogen.com*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CS0DB006YH17"
/clone_lib="LTI_NFL004_NBC2"
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/lab_host="DH10B"
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14; Mismatches 0;
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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/clone_lib="NMH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T] phage resistant)"
/lab_host="DH10B (T] phage resistant)
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 Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qlan, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Han, Z., Chen, Z., Hu, R. and Chen, J. Homo sapiens NPD library cDNA clones Unpublished (2000)

Contact: Qinghua Zhang Changhai Zhanghai Institute of Endocrinology, Rui-Jin Hospital 197 Rui-Jin II Road, Shanghai 200025, P. R. China Tel: 86-21-64370045(ex.663332)
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 529)
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/note="vector: pME18SFL
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497; Conserv
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Email: mbshiems.stn.sh.cn
This clone is available at Shanghai Hematology Institute Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiann ui- Took North
Eukaryota; Metazoa;
Mammalia; Eutheria;
                    Homo sapiens
                                human
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Shoujing Road, Zhangjiang Hi-
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="NPDAEB10"
/clone_lib="NPD"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTBT; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5: adaptor: GCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 154 c 145 g 198 t
                                GI:10735167
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GTCAATGTCTATGGTGTTGTGAAGTTCTTTAAGCCCCCCATATCTAAGCAAAGGAACTGAT 215
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702; Conserv
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Tissue procurement: ATCC/DCTD/D
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can |
found through the I.M.A.G.E. Consortium/LLNL at: image.linl.
plate: LLCM830 row: e column: 14
High quality sequence start: 52
High quality sequence stop: 746.
Location/Qualifiers
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Contact: Robert Strausberg,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/tlssue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
XhoI; S
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/db_xref="taxon:9606"
/clone="IMAGE:3955573"
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l.9e-122;
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Plate: LLAM11258 row: h column:
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Location/Qualifiers
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Tissue Procurement: ATCC
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84; Conservative
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255 c 240 g 311 t
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
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/db_xref="taxon:9606"
/clone="IMAGE:5106881"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BE884820
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information
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National Institutes of Health, Mammalian
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/clone_lib="NIH_MGC_71"
/clone_lib="NIH_MGC_71"
/tissue_type-"leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 116 c 105 g 160 t
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/db_xref="taxon:9606"
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                                                                                                                                                      TCAGAAGTTCTGATGGATGATGACCTTCAGAAAAGTGTGGRTATGATCA
                                                        ggaacaggagtactagaagcctatctcatggattctgacaaattcttccagattccagca
                                                                                                                             CCATTTCTTATACAAGGAACAATACATCACTATGGATGTAAACAGTGTTCTAGTTTGAGA
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http://fulllength.invitrogen.com"
a 176 c 166 g 256 t
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89.8%;
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Pred. No. 7.3e-159;
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nes 679; Conserv
CCACAAAATGGTAGAAGCCTTACGTGTTTTGGGCATCTACTCATATGTCACCGTCTTGGAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                    TTTGGGAGCCCCTATCATACCTCGCACTTCAAGCAAGTATTTTAACTTCACTACTGAGGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9743 row: j column: 20
High quality sequence stop: 636.
Location/Qualifiers
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BE891252
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601432077F1 NIH_MGC_72 Homo
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/db_xref='taxon:9606'
/clone='Ib='NMAGE:3917299"
/clone=lib='NH_MGC_72'
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host='DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCWV-SPORT6; Site_1: N
Site_2: Sall; Cloned unidirectionally. Primer: Ol
Average insert size 2 kb. Library constructed by
Technologies."
Technologies."
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Pred. No. 1.3e-137;
0; Mismatches 38;
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US-08-413-118-72
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                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                TELEFAX: (212) 840-071
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAOLETTI, ENGL
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: UCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AN
128
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APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                             NAME: FROMMER, WILLIAM S. REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                     LENGTH:
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                 atctgcaaatttgacagccaatcagcattcagatgttatctgtcaatcagaacctgacga 938
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                                                          Score 33.2; DE Pred. No. 8.8; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tartaglia, James
APPLICANT: Taylor, Jill
TITLE OF INVENTION: PCXVIRUS
TITLE OF INVENTION: RECOMBINA
TITLE OF INVENTION: RECOMBINA
NUMBER OF SEQUENCES: 122
                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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               SEQUENCE CHARACTERISTICS:
                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                              NAME: Frommer, William REGISTRATION NUMBER: 25
                                                                                                                                                                                                APPLICATION NUMBER: US/08/224,657 FILING DATE: 06-APR-1994
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                              TELEFAX:
                                                                                                                                                                                  CLASSIFICATION:
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5756102
                                              (: (212) 840-0712
425066 CURTMS
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3659 base pairs
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US-09-073-898-20
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                                                                                                                                                            Sequence 20, Application US/09073898 Patent No. 6242669
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                                                                                                                                               GENERAL INFORMATION:
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 20:
                                                                    APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
                      APPLICANT
                                     APPLICANT:
                                                       APPLICANT:
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LENGTH: 1045 base pair
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APPLICATION NUMBER: US 60
FILLING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Local Similarity 49.4%;
hes 86; Conservative
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
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                                                                                                                                                                                                                                                                  TTATTTAAAATAAATAGTCAAAAAACAATCTCAGCAAGTGCAACAAGACGAATTG 418
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                Loewer, David
Dullum, Charles Joseph
                                                    Stockhoff, Brian A. Schmeits, James
                                                                                       Schnepf, H. Ernest
Narva, Kenneth E.
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Muller-Cohn, Judy
                                                                                                                          Feitelson, Jerald S.
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SYSTEM: PC-DOS/MS-DOS
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Sequences Which Encode These Toxins
134
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Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.2; DB 4;
Pred. No. 5.2;
0; Mismatches 88;
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                                                                                     Sequence 72, Application US/08220151
Patent No. 5529780
GENERAL INFORMATION:
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Best Local Similarity 49.4%;
Matches 86; Conservative
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
            APPLICANT: Paoletti,
APPLICANT: Limbach, I
TITLE OF INVENTION: I
TITLE OF INVENTION: (
                                                                                                                                                                                                                                                     1405 aagtttaatagtgtaatteetgtgagatetggeeacgaagacetgggaacttttg 1458
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/029,848 FILING DATE: 30-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                 305
                                                                                                                                                                                                                                                                                                                                                                                         245 CAAAAAGGCCCAAAAGAAACAAGTTGTTCATTTAGAAAAAAGATAAATTAGTTCCCCATCAAA 304
                                                                                                                                                                                                                              365 TTATTTAAAATAAATAGTCAAAAAACAATCTCAGCAAGTGCAACAAGACGAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                     Paoletti, Enzo
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Keith J.

NUCLEOTIDE AND AMINO ACID SEQUENCES OF
CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
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US-08-836-325-14
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               GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: N-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Us
                                                                                                                                                                                                        Sequence 14, Application US/08836325 Patent No. 6110672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHANACTERISTICS:
LENGTH: 6371 base pairs
                                                                                                                                                                                                                                                                                                                 2440 AATATTTTTGACA 2452
                                                                                                                                                                                                                                                                                                                                                                             2380 GCTGAAATGGTATTAAAACTGATTGCCATGGATCCATATGAGTATTTCCAAGTAGGCTGG 2439
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APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  439 tcttggacattactaaaattgtgtgatgttcagccaatgcagtattttgacctgacttgt 498
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FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.4 hes 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/1
FILING DATE: 02-NOV-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: DC
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STREET: 1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                        cagctcttgggca 511
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ADDRESS:
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Pred. No. 7.6;
0; Mismatches 62;
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Patent No. 6204435
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                                                                                                                                            GENERAL INFORMATION:
                                               APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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FILING DATE: 02 NOV-1995
PRIOR APPLICATION DATA: 08/482,401
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/ACENT INFORMATION:
NAME: Ludwig, Steven R:
    APPLICANT:
                                    APPLICANT:
                                                                                                                                                                                                                                                    2473 AATATTTTGACA 2485
                                                                                                                                                                                                                                                                                                      2413 GCTGAAATGGTATTAAAACTGATTGCCATGGATCCATATGAGTATTTCCAAGTAGGCTGG 2472
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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REGISTRATION NUMBER: 3
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C STREET: 1100 New York Ave., N. W., Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                       Application US/08960780
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6404 base pairs
                                                            Schmeits, James
                                                                           Stockhoff, Brian A
                                                                                            Narva,
                                                                                                         Schnepf, H. Ernest
                                                                                                                         Feitelson, Jerald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                            Kenneth E.
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Pred. No. 7
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6204435el Pesticidal Toxins and Nucleotide

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                                                 Matches
                                                             Query Match
Best Local :
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Patent No. 6
                                                                                                                                                                                                       TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-960-780-41
1285 caaaaaggacgaaaagtagcagttcattttgtgaaaaataatggtattctccccgctttca 1344
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                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MA-708
TELECOMOUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPAX: 352-373-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dullum, Chaires, APPLICANT: Muller-Cohn, Judy
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
KEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                Local Similarity hes 87; Conserv
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                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                  TELEPHONE: 352-372-5800
                                                                                                                            INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible operATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Gainesville
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                                                                                                                                                                                                     1046 base pairs
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2421 N.W. 41st Street, Suite A-1
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                                              Conservative
                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feitelson, Jerald
                                                                                                                                                  DNA (genomic)
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                                                        1.9%;
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                                                     Score 34.8; D
Pred. No. 1.8;
                                           Mismatches
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                                         Indels
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US-09-073-898-41
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US-09-073-898-41
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                                                                        TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,35
REFERENCE/DOCKET NUMBER: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41,
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                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION UNATA:
APPLICATION UNBER: US 08/960,780
FILING DATE: 30-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/073,898
                                               MOLECULE TYPE:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ATTGAATATCAATCTGATAAAGCGTTAAACCCAGACAGTCAAATGTTTAAAGAATTGAAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TTATTTAAAATAAATAGTCAAAAACAATCTCAGCAAGTGCAACAAGACGAATTG 418
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            NDIVIDUAL ISOLATE: 197T1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2421 N.W. CITY: Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32606-6669
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Stamp, Lisa
Morrill, George
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Stockhoff, Brian A.
Schmeits, James
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Dullum, Charles Joseph
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                                           DNA (genomic)
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                                                                                                                                                                                                                                     39,355
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Query Match Best Local Similarity

1.9%;

Score 34.8; D Pred. No. 1.8;

DB 4;

Length 1046;

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; MOLECULE TYPE: protein US-08-852-091-4
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US-08-852-091-4
                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/852,091
PILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
PILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
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                                     269 TSYGRGIRVLPE---SNSDVDQLKK-----DLESANLTANQHSDVICQSEPDDSFPNGVS 320
                                                                            358 LKVKVL-FDKDVNERNTVKGFRKFNILGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAG 416
                                                                                                     216 LTIDILYYDNHYHVARSLKYGSFLRIYSLHTKLQSMNSENQTMLSLEF-HL-----HGG 268
                                                                                                                                                         301 LWDRT---FSLFQQLIQSSEVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYN 357
                                                                                                                                                                                                183 VWDGTRTPFPSWRVLIQD------ 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FÜNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS NOMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
    417 TRINEGPLIVIEELHSLSRETQLCQPGLVIDLETTSLPV----
                                                                                                                                                                                                                                         4.7%; Score 84; DB 2; Length 750; Local Similarity 23.9%; Pred. No. 3.8; tes 47; Conservative 28. vi.--.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 QLPSGWASILWYNMLVA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
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Curt M. Horvath
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                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                   Matches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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PRIUR APPLICATION DATA:
APPLICATION NUMBER: US 0
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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STREET: Hackensack
CITY: Hackensack
STATE: New Jersey
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301 LWDRT---FSLFQQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYN 357
                                                                           183 VWDGTRTPFPSWRVLIQD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19-MAI
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                                                                                                                                               Conservative
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19-MAR-1997
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                                                                                                                                               28;
                                                                                                                                                                            Score 84;
Pred. No.
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                                                                                                                                               Mismatches
                                                                    -----LVLEGDLSHIHRLQ-----N 215
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                                                                                                                                                                                                         Length 750;
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Query Match
Best Local Similarity
Watches 47; Conserve
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GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/369,796
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: James E. Darnell
APPLICANT: Zilong Wen
APPLICANT: Curt H. Horvath
APPLICANT: Zhong Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS RUBBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 LTIDILVYDNHVHVARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEF-HL-----HGG 268
                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-JAI CLASSIFICATION:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 28-DEC CLASSIFICATION:
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411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                         06-JAN-1995
                                                                                                                                                                                                                                                                     28-DEC-1995
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                                                                                                                                                                                                                                                                                     PCT/US95/17025
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US-08-276-099A-12
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-17025-6
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Best Local Similarity
Matches 47; Conserv
                                                                                                           TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,099A
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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NAME: Osman, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
MOLECULE TYPE: -276-099A-12
                                                                                                                                                                                       TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND TITLE OF INVENTION: BINDING ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McKnight, Ste
APPLICANT: Hou, Jinzhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 LKVKVL-FDKDVNERNTVKGFRKFNILGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAG 416
                                                 TYPE: amino ac
STRANDEDNESS:
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                                                         LENGTH: 740 ...
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                     TOPOLOGY:
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                                                                                       740 amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                       linear
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                 peptide
                                                   single
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Pred. No. 3
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er, Suite 3400
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US-08-820-754-6

Application US/08820754

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463 QLPSGWASILWYNMLVA 479

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                                                                                                                                Best Local Similarity
Matches 47; Conserv
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INFORMATION FOR SEQ ID NO: 6:
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APPLICANT:
APPLICANT:
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LENGTH: 712 amino acids
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
216 LTIDILYYDNHYHVARSLKVGSFLRIYSLHTKLQSMNSENQTMLSLEF-HL-----HGG 268
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                                                       301 LMDRT---FSLFQQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYN 357
                                                                                             183 VWDGTRTPFPSWRVLIQD-----
                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0'
FILING DATE: 19-MAR-1992
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STATE: New Jersey
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                                                                                                                                Conservative
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Wen, Zilor
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23.98;
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                                                                                                                              ; Score 84; DB 2; ; Pred. No. 3.5; 28; Mismatches (
                                                                                           ------ LVLEGDLSHIHRLQ-----N 215
                                                                                                                                62; Indels
                                                                                                                                                                Length 712
                                                                                                                                60;
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; MOLECULE TYPE: protein US-08-956-652-6
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US-08-956-652-6
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GENERAL INFORMATION:
                                                                                                                     REFERENCE/DOCKET NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1694
TELEX.
                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-MAR-PRIOR APPLICATION NUMBER:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: 23-NOV-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 11-MAR-
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: RECEPTOR R
TITLE OF INVENTION: SEQUENCES
                                                                                                                                                                                                                                         FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian Yuan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                    TYPE: a
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                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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Query Match Best Local Similarity

4.78; 23.98;

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DB 3;

Length 712;

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Qy	IPRTSSKYFNFTTEDHKMVEALRVWAS
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문	LEVLIRVEHHOOOFNIKOLLNAHVVH
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¥	327 SSYARSRLIAAS 338
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Pate GEN A	Patent No. 5929033 GENERAL INFORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Corley, Neil C.
z + + +	TITLE OF INVENTION: EXTRACELLULAR MUCOUS MAIRIX TITLE OF INVENTION: GLYCOPROTEIN NUMBER OF SPOTTENTS: 3
0	DENCE ADDRESS EE: Incyte P
	174 Porter Dr.
	COUNTRY: USA
Q	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
	rn.
Ω	SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
PI	CLASSIFICATION: PRIOR APPLICATION DATA:
	APPLICATION NUMBER: FILING DATE:
ž	ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
	REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: 0F-0477 FG
T.	ION:
INFC	TELEFAX: 650-845-4166 INFORMATION FOR SEO ID NO: 1:
S	Sis
	TYPE: amino acid ,

Gaps Gaps F 164 FR 214 FR	70; Conservative 47; Mismatches 114; Indels 122; Ga 1 MSLVPATNYIYTPLNOLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTN 1	on US/09308375 International, Inc. proteases From Gram-14-PCT VA-PCT NUMBER: US/09/308,37:1999-05-14 NUMBER: EP9719636.4 1997-09-15 13 r Windows Version 3.0 subtilis subtilis	ITYGQ DLESA : - IARV	90 KETOGITSSGFASLTEGTLGAPIIPRTSSKYFNFTTEDHKMVEALRVWAST	Query Match 4.8%; Score 85; DB 2; Length 510; Best Local Similarity 20.7%; pred. No. 1.6; Matches 69; Conservative 48; Mismatches 121; Indels 96; Gaps 30 KFFKPPYLSKGTDYCSVVTIVDQTNVKLTCLLFSGNYEALPIIYKNGDIVRFHRLKIQVY 89	: STRANDEDNESS: single : TOPOLOGY: linear : IMMEDIATE SOURCE: : LIBRARY: SINTNOT13 : CLONE: 1805538 US-09-021-323-1
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